

GenCore version 5.1.3

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:40:42 ; Search time 1031.86 Seconds
(without alignments)
5753.635 Million cell updates/sec

Title: US-09-654-743-45

Perfect score: 204

Sequence: 1 gaggtttaaatagattaaaac.....ccccaaattgcagattttac 204

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl:*

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39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	DB ID	Description
1	100.0	204	1659	6	E31042 Method for
2	100.0	204	1659	9	HSU32974
3	100.0	204	2086	9	BC032729 Homo sapi
4	100.0	204	2404	6	AX429575 Sequence
5	100.0	204	2540	6	AR103281 Sequence
6	100.0	204	2540	6	AX412118 Sequence
7	100.0	204	2540	9	HSU45880
8	100.0	204	3000	6	AX412131 Sequence
9	100.0	204	5232	6	AR106397 Sequence
10	100.0	204	5232	6	AR116699 Sequence
11	100.0	204	133391	9	HSU315G1
12	100.0	204	201197	2	HS424J12
13	84.3	172	2100	6	AX412124 Sequence
14	84.3	172	2691	6	AR106400 Sequence
15	84.3	172	2691	6	AR116702 Sequence
16	84.3	172	2691	10	MMU88990
17	83.5	170.4	1988	10	MMU36842
18	82.7	168.8	2032	10	AF304333 Rattus no
19	82.7	168.8	2468	10	AB033366
20	82.7	168.8	3032	10	AF304334 Rattus no
21	82.0	167.2	1491	10	AF183429 Rattus no
22	76.9	156.8	187568	9	AP002967
23	75.2	153.4	7990	6	AX281265 Sequence
24	75.2	153.4	7990	6	AX345060 Sequence
25	75.2	153.4	7990	6	AX281266 Sequence
26	63.4	129.4	63.4	6	AX345061 Sequence
27	60.3	123	179491	2	AC020673
28	54.6	111.4	1740	5	AF451854
29	33.5	68.4	1758	6	AX370787 Sequence
30	33.5	68.4	1758	6	AX370789 Sequence
31	33.5	68.4	2032	9	AF420440 Homo sapi
32	33.5	68.4	4993	9	AF104968 Sequence
33	33.5	68.4	4993	9	AF164682
34	33.5	68.4	144301	9	AC010467
35	33.5	68.4	165662	9	AC092070 Homo sapi
36	32.8	67	3264	5	AF008592
37	32.8	67	9960	5	AF311289
38	32.5	66.4	1946	5	AF442500
39	32.5	66.4	163882	2	AL627325
40	31.3	63.8	2667	5	GGU27466
41	31.2	63.6	1218	5	AF439767
42	30.5	62.2	2416	6	AX412128 Sequence
43	30.5	62.2	2474	6	AX412126 Sequence
44	30.5	62.2	2676	6	AR106401 Sequence
45	30.5	62.2	2676	6	AR116703 Sequence

ALIGNMENTS

RESULT 1
E31042
LOCUS E31042 Method for screening substance inhibiting binding to XIAP. linear PART 18-JUN-2001
DEFINITION E31042
ACCESSION E31042
VERSION E31042.1 GI:13017307
KEYWORDS JP 1993326328-A/2.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1659)
AUTHORS Kunihiro,M.
TITLE Method for screening substance inhibiting binding to XIAP
JOURNAL Patent: JP 1993326328-A 2 26-NOV-1999;
KUNIHIO MATSUMOTO

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COMMENT
OS Unidentified
PN JP 1999326328-A/2
PD 26-NOV-1999
PF 13-MAY-1998 JP 1998130378
PR KUNITHIRO MATSUMOTO
PI G01N33/536
PC G01N33/566,A61K38/00,A61K38/00,A61K38/00,A61K38/22,
PC A61K39/395
PC A61K45/00,A61K45/00,A61K45/00,C07K7/06,C07K7/08,C07K14/47, PC
PC G01N33/536,G01N33/536,G01N33/536/C12N15/09,C12P21/08,A61K37/02,
PC A61K37/02, PC A61K37/02,
PC A61K37/02,A61K37/24,C12N15/00
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CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 82..1572.

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Db 277 TGTCATGACGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 336
QY 181 GTATCCCAAAATTCAGATTATTC 204
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Db 337 GTATCCCAAAATTCAGATTATTC 360

RESULT 2
HSU32974 1659 bp mRNA linear PRI 12-JUN-1996
LOCUS Human IAP-like protein ILP mRNA, complete cds.
DEFINITION
ACCESSION U32974
VERSION U32974.1 GI:1016687
KEYWORDS apoptosis; ring finger; zinc finger.
SOURCE
ORGANISM Homo sapiens.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1659)
Duckett,C.S., Nava,V.E., Gedrich,R.W., Clem,R.J., Van Dongen,J.L.,
Guillilan,M.C., Shiels,H., Hardwick,J.M. and Thompson,C.B.
A conserved family of cellular genes related to the baculovirus iap
gene and encoding apoptosis inhibitors
EMBO J. 15 (11), 2685-2694 (1996)
JOURNAL 96256286
MEDLINE 8634366
PUBMED
REFERENCE
2 (bases 1 to 1659)
Duckett,C.S. and Thompson,C.B.
Direct Submission
AUTHORS
TITLE
Submitted (01-AUG-1995) Colin Duckett, Howard Hughes Medical
Institute, The University of Chicago, 924 East 57th Street,
Chicago, IL 60637, USA
JOURNAL Location/Qualifiers
1..1659
/organism="Homo sapiens"

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Db 337 GTATCCCAAAATTCAGATTATTC 360

RESULT 3
BC032729 2086 bp mRNA linear PRI 27-JUN-2002
LOCUS Homo sapiens, baculoviral IAP repeat-containing 4, clone MGC:45369
DEFINITION
IMAGE:5532247, mRNA, complete cds.
ACCESSION BC032729
VERSION BC032729.1 GI:21619763
KEYWORDS MGC.
human.
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2086)
Straussberg,R.
Direct Submission
AUTHORS
TITLE
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
CONTACT: MGC help desk
COMMENT Email: cgapbs@mail.nih.gov

```

Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC),
Gaithersburg, Maryland;
Web site: <http://www.nisc.nih.gov/>
Contact: nisc.mc@nih.gov
Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
McDowall, J., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
Madwell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 69 Row: j Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4502142.

FEATURES
source
1. 2086
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Qy 121 TGTCTATGAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTGGGAAGACACAGGAAA 180
Db 274 TGTCTATGAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTGGGAAGACACAGGAAA 333
Qy 181 GTATCCCAAAATTCGAGATTATC 204
Db 334 GTATCCCAAAATTCGAGATTATC 357
RESULT 4
AX429575
LOCUS 2404 bp DNA linear PAT 21-JUN-2002

DEFINITION Sequence 38 from Patent WO0226820.
ACCESSION AX429575
VERSION AX429575.1 GI:21540833
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Cohen, D., Dengler, U.J., Finelli, A.L., Freuler, F., Konsolaki, M.,
Reinhardt, M.W. and Zusman, S.
TITLE Transgenic drosophila melanogaster expressing beta amyloid
JOURNAL Patent: WO 0226820-A 38 04-APR-2002;
NOVARTIS ERFIND VERWALT GMBH (AT)
FEATURES Location/Qualifiers
source 1..2404
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Qy 61 ACACCTGGCAGCAGCAGGGTTCCTTTTATCTGTTGAAGAGATACCGTGGGTCCTTTAGT 120
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Db 229 TGTCTATGAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTGGGAAGACACAGGAAA 288
Qy 181 GTATCCCAAAATTCGAGATTATC 204
Db 289 GTATCCCAAAATTCGAGATTATC 312
RESULT 5
LOCUS AR103281 2540 bp DNA
DEFINITION Sequence 1 from patent US 6087173.
ACCESSION AR103281
VERSION AR103281.1 GI:12814869
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2540)
AUTHORS Bennett, C.Frank., Ackermann, E.J. and Cowser, L.M.
TITLE Antisense modulation of X-linked inhibitor of apoptosis expression
JOURNAL Patent: US 6087173-A 1 11-JUL-2000;
FEATURES Location/Qualifiers
source 1..2540
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 Qy 181 GTATCCCCAAATTCAGATTATC 204
 Db 289 GTATCCCCAAATTCAGATTATC 312

RESULT 6
 AX412118
 LOCUS AX412118 2540 bp DNA linear PAT 14-JUN-2002
 DEFINITION Sequence 218 from Patent WO0226968.
 ACCESSION AX412118
 VERSION AX412118.1 GI:21444581
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.
 Antisense lrp nucleic acids and uses thereof
 Patent: WO 0226968-A 218 04-APR-2002;
 University of Ottawa (CA); Aegera Therapeutics Inc. (CA)
 FEATURES
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 Qy 181 GTATCCCCAAATTCAGATTATC 204
 Db 289 GTATCCCCAAATTCAGATTATC 312

RESULT 7
 HSU45880
 LOCUS HSU45880 2540 bp mRNA linear PRI 16-FEB-1996
 DEFINITION Human X-linked inhibitor of apoptosis protein XIAP mRNA, complete
 cds.
 ACCESSION U45880
 VERSION U45880.1 GI:1184319
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2540)
 Liston, P., Roy, N., Tamai, K., Lefebvre, C., Baird, S.,
 Cherton-Horvat, G., Farahani, R., McLean, M., Ikeda, J., Mackenzie, A.
 and Korneluk, R.G.
 TITLE Suppression of apoptosis in mammalian cells by NAIP and a related
 family of IAP genes
 JOURNAL Nature 379 (6563), 349-353 (1996)

96149249
 8552191
 2 (bases 1 to 2540)
 Baird, S.D.
 Direct Submission
 Submitted (16-JAN-1996) Stephen D. Baird, Children's Hospital of
 Eastern Ontario, Genetics, 401 Smyth Rd., Ottawa, Ontario, K1H 8L1,
 Canada
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RESULT 8
 AX412131
 LOCUS AX412131 3000 bp DNA linear PAT 14-JUN-2002
 DEFINITION Sequence 231 from Patent WO0226968.
 ACCESSION AX412131
 VERSION AX412131.1 GI:21444588
 KEYWORDS human.

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.
TITLE Antisense iap nucleic acids and uses thereof
JOURNAL Patent: WO 0226968-A 231 04-APR-2002;
University of Ottawa (CA); Aegera Therapeutics Inc. (CA)

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QY 181 GTATCCCAAAATTCAGATTATC 204
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Db 945 GTATCCCAAAATTCAGATTATC 968
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RESULT 9
ARI06397
LOCUS ARI06397 5232 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6107041.
ACCESSION ARI06397
VERSION ARI06397.1 GI:12820927
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 5232)
AUTHORS Korneluk, R.G., MacKenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease
JOURNAL Patent: US 6107041-A 3 22-AUG-2000;
Location/Qualifiers
Source 1..5232
/organism="unknown"

BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others
ORIGIN

Query Match 100.0%; Score 204; DB 6; Length 5232;
Best Local Similarity 100.0%; Pred. No. 3.3e-50;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAATAAACTTTTCTTAATTTCCCAAGTGGTAGTCTCTGTTTCAGCATCA 60
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Db 109 GAGTTTAATAGATTAATAAACTTTTCTTAATTTCCCAAGTGGTAGTCTCTGTTTCAGCATCA 168
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QY 61 ACAGTGGCAGCAGCAGGGTTCTTTTACTGTTGAAGGAGATACCGTGGGTCCTTTAGT 120
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Db 169 ACAGTGGCAGCAGCAGGGTTCTTTTACTGTTGAAGGAGATACCGTGGGTCCTTTAGT 228
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QY 121 TGTCTATGACGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTGGGAAGACACAGGAAA 180
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Db 229 TGTCTATGACGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTGGGAAGACACAGGAAA 288
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QY 181 GTATCCCAAAATTCAGATTATC 204
|||||
Db 289 GTATCCCAAAATTCAGATTATC 312
|||||

RESULT 11
HSDJ315G1
LOCUS HSDJ315G1 133391 bp DNA linear PRI 23-JUN-2000
DEFINITION Human DNA sequence from clone Rpl-315G1 on chromosome Xq24-25.
Contains a PDZ (DHR, GLGF) domain protein pseudogene, the API3 gene for apoptosis inhibitor 3 (XIAP, HILP), a putative novel gene, ESTs, SPSSs, GSSs and a putative CpG island, complete sequence.

ACCESSION AL121601
VERSION AL121601.13 GI:7159760
KEYWORDS HTG; API3; CpG island; DHR; GLGF; HILP; PDZ; XIAP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 133391)
AUTHORS Direct Submission
TITLE Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT On Mar 6, 2000 this sequence version replaced gi:6983378.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission

QY 181 GTATCCCAAAATTCAGATTATC 204
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Db 289 GTATCCCAAAATTCAGATTATC 312
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RESULT 10
ARI16699
LOCUS ARI16699 5232 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6133437.
ACCESSION ARI16699
VERSION ARI16699.1 GI:14097021
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 5232)
AUTHORS Korneluk, R.G., MacKenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.
TITLE Modulation of IAPs for the treatment of proliferative diseases
JOURNAL Patent: US 6133437-A 3 17-OCT-2000;
Location/Qualifiers
Source 1..5232
/organism="unknown"

BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others
ORIGIN

Query Match 100.0%; Score 204; DB 6; Length 5232;
Best Local Similarity 100.0%; Pred. No. 3.3e-50;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAATAAACTTTTCTTAATTTCCCAAGTGGTAGTCTCTGTTTCAGCATCA 60
|||||
Db 109 GAGTTTAATAGATTAATAAACTTTTCTTAATTTCCCAAGTGGTAGTCTCTGTTTCAGCATCA 168
|||||

QY 61 ACAGTGGCAGCAGCAGGGTTCTTTTACTGTTGAAGGAGATACCGTGGGTCCTTTAGT 120
|||||
Db 169 ACAGTGGCAGCAGCAGGGTTCTTTTACTGTTGAAGGAGATACCGTGGGTCCTTTAGT 228
|||||

QY 121 TGTCTATGACGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTGGGAAGACACAGGAAA 180
|||||
Db 229 TGTCTATGACGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTGGGAAGACACAGGAAA 288
|||||

QY 181 GTATCCCAAAATTCAGATTATC 204
|||||
Db 289 GTATCCCAAAATTCAGATTATC 312
|||||

RESULT 11
HSDJ315G1
LOCUS HSDJ315G1 133391 bp DNA linear PRI 23-JUN-2000
DEFINITION Human DNA sequence from clone Rpl-315G1 on chromosome Xq24-25.
Contains a PDZ (DHR, GLGF) domain protein pseudogene, the API3 gene for apoptosis inhibitor 3 (XIAP, HILP), a putative novel gene, ESTs, SPSSs, GSSs and a putative CpG island, complete sequence.

ACCESSION AL121601
VERSION AL121601.13 GI:7159760
KEYWORDS HTG; API3; CpG island; DHR; GLGF; HILP; PDZ; XIAP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 133391)
AUTHORS Direct Submission
TITLE Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,
JOURNAL CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT On Mar 6, 2000 this sequence version replaced gi:6983378.
During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission

corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated human repeat sequence elements (e.g. Alu). Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key.

The following abbreviations are used to associate primary accession numbers given in the evidence table with their source databases: pm, EMBL; Sw, SWISSPROT; Tr, TrEMBL; Wp, WormPEP; Information by the WormPEP database can be found at

http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence was generated from part of bacterial clone contigs of human chromosome X, constructed by the Sanger Centre Chromosome X Mapping Group. Further information can be found at

<http://www.sanger.ac.uk/HGP/ChrX>

RPI-315G1 is from the library RPCI-1 constructed at the Roswell Park Cancer Institute by the group of Pieter de Jong. For further details see <http://bacpac.med.buffalo.edu/>

VECTOR: pCYPAC2

This sequence is the entire insert of clone RPI-315G1 The true right end of clone RP6-30A23 is at 100 in this sequence.

FEATURES

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   /clone_lib="RPCI-1"
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   complement(4112..4623)
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   4617..5326
   /note="match: GSS: Em:AQ740042"
   4624..4824
   /note="match: GSS: Em:AQ587673"
   4828..5111
   /note="match: GSS: Em:AQ587673"
   complement(6712..7417)
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   /note="dJ315G1.1 (PDZ (DHR, GLGF) domain protein
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   match: proteins: Tr:O9Y510 Tr:O14911 Tr:O9Z101 Tr:O18129
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   /note="match: GSS: Em:AQ740042"
   4624..4824
   /note="match: GSS: Em:AQ587673"
   4828..5111
   /note="match: GSS: Em:AQ587673"
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   pseudogene)
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   match: proteins: Tr:O9Y510 Tr:O14911 Tr:O9Z101 Tr:O18129
   Tr:O97111"
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match: proteins: Tr:O9Y510 Tr:O14911 Tr:O9Z101 Tr:O18129
Tr:O97111"
/pseudo
/codon_start=1
/evidence=not_experimental
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28615..28815,35110..36179)
/gene="API3"
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/note="match: CDNAS: Em:AB033366 Em:U88990 Em:U32974
Em:U45880 Em:U36842
match: ESTs: Em:HSCZOG051 Em:AI628066 Em:AA295472
Em:AI598959 Em:AI418337 Em:AI277821 Em:HSCZOG052
Em:AA987840"
/evidence=not_experimental
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28615..28815,35110..35303)
/gene="API3"
/note="match: proteins: Tr:O57319 Sw:P98170 Sw:Q90660
Sw:Q13490 Sw:Q60989 Sw:Q62210"
/codon_start=1
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/product="dJ315G1.2 (apoptosis inhibitor 3 (XIAP, HILP))"
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CDS

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   /db_xref="taxon:9606"
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   /map="q24-q25"
   /clone="RPI-315G1"
   /clone_lib="RPCI-1"
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   complement(4112..4623)
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   4617..5326
   /note="match: GSS: Em:AQ740042"
   4624..4824
   /note="match: GSS: Em:AQ587673"
   4828..5111
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   complement(6712..7417)
   /gene="dJ315G1.1"
   complement(6712..7417)
   /gene="dJ315G1.1"
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   /note="dJ315G1.1 (PDZ (DHR, GLGF) domain protein
   pseudogene)
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   match: proteins: Tr:O9Y510 Tr:O14911 Tr:O9Z101 Tr:O18129
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/note="90 copies 2 mer ta 73% conserved"
complement(28616..28815)
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29663..29811
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31721..31780
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complement(69632..69793)
/note="match: GSS: Em:AQ380019"
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Best Local Similarity 100.0%; Pred. No. 4.1e-50;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 61 ACATGCGCAGCAGCAGGTTTCTTATCTGTTGAAGAGATACCGTGGTGGCTTTAGT 120
Db 13920 ACATGCGCAGCAGCAGGTTTCTTATCTGTTGAAGAGATACCGTGGTGGCTTTAGT 13979

Qy 121 TGTATGACGCTGTAGATAGATGCAATATGAGACTCAGCAGTGGAGACACAGGAAA 180
Db 13980 TGTATGACGCTGTAGATAGATGCAATATGAGACTCAGCAGTGGAGACACAGGAAA 14039

Qy 181 GTATCCCAAAATGCGAGATTATC 204
Db 14040 GTATCCCAAAATGCGAGATTATC 14063

RESULT 12
HS424J12          201197 bp   DNA   linear   HTG 10-JUL-2001
LOCUS             Homo sapiens chromosome X clone RP3-424J12, *** SEQUENCING IN
DEFINITION        PROGRESS ***, 15 unordered pieces.
ACCESSION          Z82207
VERSION            Z82207.3   GI:12331276
KEYWORDS           HTG; HTGS-PHASE1; HTGS-CANCELLED.
SOURCE             human.
ORGANISM           Homo sapiens
                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                   Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE          1 (bases 1 to 201197)
AUTHORS            Graham,D.
TITLE              Direct Submision
JOURNAL            Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
                   CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone
                   requests: clonerequest@sanger.ac.uk
COMMENT            On Jan 22, 2001 this sequence version replaced gi:10045116.
                   ----- Genome Center

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Center: Sanger Centre
Center code: SC
Web site: http://www.sanger.ac.uk
Contact: humquery@sanger.ac.uk
----- Project Information
Center project name: dj424J12
----- Summary Statistics
Assembly program: XGAP4; version 4.5
Sequencing vector: M13; M7815; 74% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Chemistry: Dye-terminator ABI; 96% of reads
Chemistry: Dye-primer-amersham; 2% of reads
Chemistry: Dye-primer Big Dye; 0% of reads
Consensus quality: 194333 bases at least Q40
Consensus quality: 196512 bases at least Q30
Consensus quality: 198047 bases at least Q20
Insert size: 199797; sum-of-contigs
Quality coverage: 6.87x in Q20 bases; sum-of-contigs
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* NOTE: This is a 'working draft' sequence. It currently
* consists of 15 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 4154: contig of 4154 bp in length
* 4155 4254: gap of 100 bp
* 4255 18703: contig of 14449 bp in length
* 18704 18803: gap of 100 bp
* 18804 20941: contig of 2138 bp in length
* 20942 21041: gap of 100 bp
* 21042 34907: contig of 13866 bp in length
* 34908 35012: gap of 105 bp
* 35013 37508: contig of 2496 bp in length
* 37509 37608: gap of 100 bp
* 37609 52739: contig of 15131 bp in length
* 52740 52839: gap of 100 bp
* 52840 56933: contig of 4094 bp in length
* 56934 57033: gap of 100 bp
* 57034 88245: contig of 31212 bp in length
* 88246 88346: gap of 101 bp
* 88347 93386: contig of 5040 bp in length
* 93387 93486: gap of 100 bp
* 93487 123956: contig of 30470 bp in length
* 123957 124056: gap of 100 bp
* 124057 147917: contig of 23861 bp in length
* 147918 148017: gap of 100 bp
* 148018 176236: contig of 28219 bp in length
* 176237 176336: gap of 100 bp
* 176337 187128: contig of 10792 bp in length
* 187129 187228: gap of 100 bp
* 187229 190824: contig of 3596 bp in length
* 190825 190959: gap of 135 bp
* 190960 201197: contig of 10238 bp in length.
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FEATURES
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misc_feature

misc_feature

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176337..187128
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187229..190824
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 4.2e-50;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
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Db 42632 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 42691
QY 61 ACACGTGGCAGCAGCGGGTCTTTTACTGCTGAGGAGATACCGTGGGTCCTTTAGT 120
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Db 42752 TGTCTATGACGCTGTAGATAGATGCGCAATATGAGACTTCAGCAGTGGGAAGACACAGGAAA 42811
QY 181 GTATCCCCAAATTCGAGATTATC 204
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Db 42812 GTATCCCCAAATTCGAGATTATC 42835

RESULT 13
LOCUS AX412124 2100 bp DNA linear PAT 15-JUN-2002
DEFINITION Sequence 224 from Patent WO0226968.
ACCESSION AX412124
VERSION AX412124.1 GI:21444584
KEYWORDS house mouse.
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Korneluk,R.G., Lacasse,E., Baird,S., Holcik,M. and Young,S.
TITLE Antisense iap nucleic acids and uses thereof
JOURNAL Patent: WO 0226968-A 224 04-APR-2002;
University of Ottawa (CA); Aegera Therapeutics Inc. (CA)
FEATURES
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BASE COUNT 615 a 417 c 482 g 586 t
ORIGIN

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Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
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Db 202 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 261
QY 61 ACACGTGGCAGCAGCGGGTCTTTTACTGCTGAGGAGATACCGTGGGTCCTTTAGT 120
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Db 262 ACATTTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGGCAATGTTTCAGT 321
QY 121 TGTCTATGACGCTGTAGATAGATGCGCAATATGAGACTTCAGCAGTGGGAAGACACAGGAAA 180
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QY 181 GTATCCCCAAATTCGAGATTATC 204
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Db 382 ATATCCCCAAATTCGAGATTATC 405
RESULT 14
LOCUS AR106400 2691 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6107041.
ACCESSION AR106400
VERSION AR106400.1 GI:12820930
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Korneluk,R.G., Mackenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease
JOURNAL Patent: US 6107041-A 9 22-AUG-2000;
FEATURES Location/Qualifiers
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/organism="unknown"
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Best Local Similarity 90.2%; Pred. No. 1.2e-40;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
|||||
Db 747 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 806
QY 61 ACACGTGGCAGCAGCGGGTCTTTTACTGCTGAGGAGATACCGTGGGTCCTTTAGT 120
|||||
Db 807 ACATTTGGCGGAGCTGGGTTCTTTTATACCGGTGAAGGAGACACCGTGGCAATGTTTCAGT 856
QY 121 TGTCTATGACGCTGTAGATAGATGCGCAATATGAGACTTCAGCAGTGGGAAGACACAGGAAA 180
|||||
Db 867 TGTCTATGCGGCAATAGATAGATGCGCAGTATGAGACTTCAGTCTTGGAGACACAGGAGA 926
QY 181 GTATCCCCAAATTCGAGATTATC 204
|||||
Db 927 ATATCCCCAAATTCGAGATTATC 950
RESULT 15
LOCUS AR116702 2691 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6133437.
ACCESSION AR116702
VERSION AR116702.1 GI:14097024
KEYWORDS
SOURCE Unknown.

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (Bases 1 to 2691)
AUTHORS Korneluk,R.G., MacKenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.
TITLE Modulation of IAPs for the treatment of proliferative diseases
JOURNAL Patent: US 613437-A 9 17-OCT-2000;
FEATURES Location/Qualifiers
source 1..2691
BASE COUNT 819 a 479 c 562 g 831 t
ORIGIN
Query Match 84.3%; Score 172; DB 6; Length 2691;
Best Local Similarity 90.2%; Pred. No. 1.2e-40;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
Qy 1 GAGTTTAATAGATTAAACACTTTTGCTAATTTTCCAACTGCTAGTCTCTGTTTCAGCATCA 60
Db 747 GAGTTTAATAGATTAAACACTTTTGCTAATTTTCCAACTGCTAGTCTCTGTTTCAGCATCA 806
Qy 61 ACACGTGGCAGCAGCAGGCTTTTACTGTTGAAGGAGATACCGTGGGTGCTTTAGT 120
Db 807 ACATTGGCGCGAGCTGGTCTTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 866
Qy 121 TGTCATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
Db 867 TGTCATGGCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAGACACAGGAGA 926
Qy 181 GTATCCCCAAATTGCAGATTATC 204
Db 927 ATATCCCCAAATTGCAGATTATC 950

Search completed: April 15, 2003, 23:23:15
Job time : 1070.86 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:38:17 ; Search time 136.354 Seconds

(without alignments)
3369.223 Million cell updates/sec

Title: US-09-654-743-45

Perfect score: 204

Sequence: 1 gagtttaattagattaaac.....ccccaaattgcagattttatc 204

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

Result No.	Query	Score	Match	Length	ID	Description
1	204	100.0	1659	21	AAZ48862	Human XIAP coding
2	204	100.0	2404	24	AAK99405	DNA of APP related
3	204	100.0	2540	18	AAK70836	Human apoptosis in
4	204	100.0	2540	21	AAK64901	Human X-linked inh
5	204	100.0	2540	24	ABK93869	Human cDNA encodin
6	204	100.0	3000	24	ABK93875	Human cDNA encodin
7	204	100.0	5232	19	AAV55038	Human XIAP coding
8	172	84.3	2100	18	AAK70839	Mouse apoptosis in
9	172	84.3	2100	24	ABK93872	Mouse cDNA encodin

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	172	84.3	2691	19	AAV55041	Murine XIAP coding
11	170.4	83.5	1988	18	AAK72710	Mouse inhibitor of
12	153.4	75.2	7990	24	ABL54307	Chemically treated
13	153.4	75.2	7990	24	ABL32158	Human immune syste
14	129.4	63.4	7990	24	ABL54308	Chemically treated
15	129.4	63.4	7990	24	ABL32159	Human immune syste
16	68.4	33.5	1559	24	ABK13197	Human testes speci
17	68.4	33.5	1758	24	ABK14677	Human inhibitor of
18	68.4	33.5	1758	24	ABK14678	Human inhibitor of
19	68.4	33.5	4993	22	AAK03581	Human IAP-like pro
20	62.2	30.5	2416	18	AAK70841	Mouse apoptosis in
21	62.2	30.5	2416	24	ABK93874	Mouse cDNA encodin
22	62.2	30.5	2474	18	AAK70840	Mouse apoptosis in
23	62.2	30.5	2474	24	ABK93873	Mouse cDNA encodin
24	62.2	30.5	2676	19	AAV55042	Murine HIAP-1 codi
25	62.2	30.5	2862	18	AAK61592	Murine c-IAP, Mus
26	62.2	30.5	3151	19	AAV55043	Murine HIAP-2 codi
27	58.2	28.5	794	24	ABL55635	AmEPV baculovirus-
28	58.2	28.5	50000	24	ABL55643	Human apoptosis in
29	56	27.5	2666	18	AAK70837	Human cDNA encodin
30	56	27.5	2676	24	ABK93870	Human inhibitor of
31	56	27.5	3076	18	AAK72712	Human cellular inh
32	56	27.5	3076	20	AAZ41005	Human cellular inh
33	56	27.5	3076	20	AAZ22096	Breast cancer rela
34	56	27.5	3076	24	ABL62746	Lung cancer relate
35	56	27.5	3076	24	ABL66325	Human HIAP-1 codin
36	56	27.5	6669	19	AAV55039	Human cDNA encodin
37	56	27.5	6669	24	ABK93876	Human colon cancer
38	55.8	27.4	649	24	ABQ60576	Human apoptosis in
39	55.8	27.4	2580	18	AAK70838	Human cDNA encodin
40	55.8	27.4	2580	24	ABK93871	Human c-IAP1, Hom
41	55.8	27.4	2589	18	AAK61590	Human inhibitor of
42	55.8	27.4	3532	18	AAK72711	Human cellular inh
43	55.8	27.4	3532	20	AAZ22143	Gene #3355 used to
44	55.8	27.4	3532	24	ABN96857	Human HIAP-2 codin
45	55.8	27.4	3732	19	AAV55040	

ALIGNMENTS

RESULT 1

AAZ48862

ID AAZ48862 standard; cDNA; 1659 BP.

XX AC AAZ48862;

XX DT 24-MAR-2000: (first entry)

XX DE Human XIAP coding sequence.

XX XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;

KW transforming growth factor-beta activated kinase 1; monocyte migration;

KW TAK1 binding protein 1; extracellular matrix protein production;

KW cell growth inhibitor; beta-amyloid protein deposition;

XX immunosuppression; Transforming growth factor-beta; ds.

XX OS Homo sapiens.

XX PN JP11326328-A.

XX XX 26-NOV-1999.

XX PF 13-MAY-1998; 98JP-0130378.

XX PR 13-MAY-1998; 98JP-0130378.

XX PA (MATS/) MATSUMOTO K.

XX XX WPI; 2000-078337/07.

XX DR P-PSDB; AAY59451.

XX XX Screening a substance which inhibits combination of the X-linked

PT

PT inhibitor of apoptosis protein
 PS Disclosure; Page 28-30; 43pp; Japanese.
 XX
 CC This sequence encodes the human XIAP protein.
 CC The invention relates to a method for screening a substance inhibiting
 CC the formation of a complex between XIAP and TAB1, in which X-linked
 CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta
 CC activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be
 CC tested are contacted with each other and then the presence or formation
 CC of a complex between XIAP and TAB1 is detected. The substance can be used
 CC as a drug for extracellular matrix protein production enhancement, cell
 CC growth inhibition, monocyte migration, physiologically active substance
 CC induction, immunosuppression, and beta-amyloid protein deposition. A
 CC substance inhibiting the formation of a complex between TAB1 and XIAP as
 CC well as between XIAP and TGF-beta (transforming growth factor-beta) type
 CC I and/or type II receptor is useful as a drug.
 XX
 SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;
 Query Match 100.0%; Score 204; DB 21; Length 1659;
 Best Local Similarity 100.0%; Pred. No. 8.5e-58;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 60
 Db 157 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 216
 Qy 61 ACACCTGGCAGCAGGAGGTTTCTTTATACCTGTTGAGAGATACCGTGGTGTCTTAGT 120
 Db 217 ACACCTGGCAGCAGGAGGTTTCTTTATACCTGTTGAGAGATACCGTGGTGTCTTAGT 276
 Qy 121 TGTCTATGACGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 180
 Db 277 TGTCTATGACGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 336
 Qy 181 GTATCCCCAAATTCAGATTATC 204
 Db 337 GTATCCCCAAATTCAGATTATC 360
 RESULT 2
 AAK99405
 ID AAK99405 standard; DNA; 2404 BP.
 AC AAK99405;
 XX
 XX 27-JUN-2002 (first entry)
 DE DNA of APP related human homologue hCP35211.
 XX
 KW Neuroprotective; nontropic; transgenic fly; Alzheimer's disease; Abeta;
 KW amyloid precursor protein; tissue-specific expression control; human APP;
 KW APP pathway modulator; gene therapy; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 CD 5 692..1528
 FT /tag= a
 FT /product= "Protein of human homologue hCP35211"
 FT /note= "No start codon"
 XX
 XX WO200226820-A2.
 XX
 XX 04-APR-2002.
 XX
 XX 01-OCT-2001; 2001WO-EPI1345.
 XX
 XX 29-SEP-2000; 2000US-236893P.
 XX
 XX 14-JUN-2001; 2001US-298309P.
 XX
 XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
 PI Reinhardt MWMH, Zusman S;
 XX WPT; 2002-315796/35.
 DR P-PSDB; AAO20511.
 XX
 XX New transgenic fly, containing DNA encoding an Abeta portion of human
 XX APP, useful for identifying agents which modulate the APP pathway and
 XX which can be used to treat Alzheimer's disease
 XX Example 4; Page 111; 129pp; English.
 XX
 XX The invention relates to a transgenic fly whose genome comprises DNA
 XX encoding a polypeptide having the Abeta portion of human amyloid
 XX precursor protein (APP), fused to a signal sequence. The DNA sequence
 XX encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
 XX the specification. The DNA sequence is operably linked to a tissue-
 XX specific expression control sequence. Expression of the sequence gives
 XX the fly an altered phenotype. The purpose of the invention is for
 XX identifying agents that inhibit or promote the expression and/or function
 XX of genes or encoded polypeptides which modify the APP pathway. The agent
 XX is a compound, triple helix DNA, antisense oligonucleotide, double
 XX stranded RNA molecule, ribozyme, or particularly an antibody. It is used
 XX to treat conditions such as Alzheimer's disease. The agent can be used as
 XX an APP pathway modulator or in gene therapy. This polynucleotide sequence
 XX represents the DNA of the APP related human homologue hCP35211.
 XX
 SQ Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 other;
 Query Match 100.0%; Score 204; DB 24; Length 2404;
 Best Local Similarity 100.0%; Pred. No. 1e-57;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 60
 Db 109 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 168
 Qy 61 ACACCTGGCAGCAGGAGGTTTCTTTATACCTGTTGAGAGATACCGTGGTGTCTTAGT 120
 Db 169 ACACCTGGCAGCAGGAGGTTTCTTTATACCTGTTGAGAGATACCGTGGTGTCTTAGT 228
 Qy 121 TGTCTATGACGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 180
 Db 229 TGTCTATGACGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 288
 Qy 181 GTATCCCCAAATTCAGATTATC 204
 Db 289 GTATCCCCAAATTCAGATTATC 312
 RESULT 3
 AAT70836
 ID AAT70836 standard; cDNA; 2540 BP.
 XX
 XX AAT70836;
 AC
 XX
 XX 02-SEP-1997 (first entry)
 DT
 XX
 XX Human apoptosis inhibitor xiap cDNA.
 DE
 XX
 XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
 KW XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;
 KW ischaemia; myocardial infarction; stroke;
 KW reperfusion injury; toxin-induced liver disease; gene therapy;
 KW diagnosis; ds.
 XX
 XX Homo sapiens.
 OS
 XX
 XX Key Location/Qualifiers
 FH CDS 34..1527
 FT /tag= a

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XX PN W09706255-A2.
XX PD 20-FEB-1997.
XX PF 05-AUG-1996; 96WO-IB01022.
XX PR 22-DEC-1995; 95US-0576956.
XX PR 04-AUG-1995; 95US-0511485.
XX PA (UTOT-) UNIV OTTAWA.
XX PI Baird S, Korneluk RG, Liston P, Mackenzie AB;
XX DR WPI: 1997-154262/14.
XX DR P-PSDB; AAW19581.
XX PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
XX PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
XX PT of susceptibility to apoptotic disease
XX PS Claim 12; Page 67-68; 21pp; English.
XX CC Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and
XX CC hiap-2 genes (AAW70836-41) respectively code for a new class of
XX CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis
XX CC (IAP). The xiap gene (for X-linked IAP gene) was isolated from a
XX CC human foetal brain zapfi cDNA library using an X-linked sequence
XX CC tag site that shows strong homology with the conserved ring zinc
XX CC finger domain of baculovirus CpiAP and OpiAP genes. The gene was
XX CC assigned to chromosome Xq25 by FISH. IAP nucleic acids can be used
XX CC to express IAP polypeptides in cells and animals to inhibit
XX CC apoptosis, and as primers and probes to identify and isolate
XX CC additional IAP genes, as well as in methods for treating diseases
XX CC and disorders involving apoptosis (anti-apoptotic gene therapy).
XX SQ Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 1 other;

Query Match 100.0%; Score 204; DB 18; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1e-57;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
DB 109 GAGTTTAATAGATTAAACACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 168

QY 61 ACACGTGGCAGCAGCAGGGTTTCTTTATACCTGGTGAAGGAGATACCCGTGCGGTGCTTTAGT 120
DB 169 ACACGTGGCAGCAGCAGGGTTTCTTTATACCTGGTGAAGGAGATACCCGTGCGGTGCTTTAGT 228

QY 121 TGTCTATGCAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTTCGGAACACACAGGAAA 180
DB 229 TGTCTATGCAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTTCGGAACACACAGGAAA 288

QY 181 GATATCCCAAAATTCGAGATTATC 204
DB 289 GATATCCCAAAATTCGAGATTATC 312

RESULT 4
ID AAA64901
XX: AAA64901
AC: AAA64901;
XX:
XX: 07-NOV-2000 (first entry)
XX: Human X-linked inhibitor of apoptosis DNA.
XX: X-linked inhibitor of apoptosis; XIAP; hIAP; MIHA; U45880;
XX: antisense; antiinflammatory; cytostatic; tumour; ds.
XX: Homo sapiens.
OS:

```

```

XX FH Key Location/Qualifiers
XX CDS 34..1527
XX FT /*tag= a
XX FT /product= "X-linked inhibitor of apoptosis"
XX PN USG087173-A.
XX PD 11-JUL-2000.
XX PF 09-SEP-1999; 99US-0392580.
XX PR 09-SEP-1999; 99US-0392580.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Cowser LM, Ackermann EJ;
XX DR WPI: 2000-498201/44.
XX DR P-PSDB; AAY99985.
XX PT Antisense compound useful for research reagents, diagnostics,
XX PT prophylaxis and for treating disorders associated with X-linked
XX PT inhibitor of apoptosis, modulates expression of X-linked inhibitor of
XX PS apoptosis
XX PS Example 13; Column 43-48; 33pp; English.
XX CC The present invention relates to antisense oligonucleotides designed to
XX CC inhibit expression of the human X-linked inhibitor of apoptosis. The
XX CC present sequence is the X-linked inhibitor of apoptosis DNA.
XX CC Modified phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are
XX CC more effective inhibitors than unmodified oligonucleotides. The
XX CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
XX CC expression in cells and tissues in vitro. The oligonucleotides are also
XX CC useful for treating animals or humans, prone to a disease associated
XX CC with X-linked inhibitor of apoptosis. The oligonucleotides may also be
XX CC used prophylactically to prevent infection, inflammation or tumour
XX CC formation.
XX SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 other; 1

Query Match 100.0%; Score 204; DB 21; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1e-57;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
DB 109 GAGTTTAATAGATTAAACACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 168

QY 61 ACACGTGGCAGCAGCAGGGTTTCTTTATACCTGGTGAAGGAGATACCCGTGCGGTGCTTTAGT 120
DB 169 ACACGTGGCAGCAGCAGGGTTTCTTTATACCTGGTGAAGGAGATACCCGTGCGGTGCTTTAGT 228

QY 121 TGTCTATGCAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTTCGGAACACAGGAAA 180
DB 229 TGTCTATGCAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTTCGGAACACAGGAAA 288

QY 181 GATATCCCAAAATTCGAGATTATC 204
DB 289 GATATCCCAAAATTCGAGATTATC 312

RESULT 5
ID ABK93869
XX: ABK93869 standard; cDNA; 2540 BP.
XX:
XX: AC ABK93869;
XX:
XX: 26-AUG-2002 (first entry)
XX: Human cDNA encoding inhibitor of apoptosis, XIAP #1.
XX:
XX:

```


KW Human; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX Homo sapiens.
 XX WO200226968-A2.
 PN 04-APR-2002.
 PD 27-SEP-2001; 2001WO-CA01379.
 XX 28-SEP-2000; 2000US-0672717.
 PR (UYOT-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 PI P-PSDB; ABG65663.
 DR WPI; 2002-479562/51.
 DR P-PSDB; ABG65663.
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for
 PT enhancing apoptosis in a cell, for treating cancer and other
 PT proliferative diseases -
 XX Disclosure; Fig 1; 135pp; English.
 XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC cDNA sequence.
 XX Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;
 SQ
 Query Match 100.0%; Score 204; DB 24; Length 2540;
 Best Local Similarity 100.0%; Pred. No. 1e-57;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAGTTTAATAGATTAAACACTTTTCTATATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 50
 DB 109 GAGTTTAATAGATTAAACACTTTTCTATATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 168
 QY 61 ACACCTGGCAGCAGCGGGTTTCTTATCTGTTGAAGAGATACCGTGGGTCTTTAGT 120
 DB 169 ACACCTGGCAGCAGCGGGTTTCTTATCTGTTGAAGAGATACCGTGGGTCTTTAGT 228
 QY 121 TGTCTATGACGTGTAGATAGATGGCAATATGAGACTCAGCAGTTTGGAGACACAGGAAA 180
 DB 229 TGTCTATGACGTGTAGATAGATGGCAATATGAGACTCAGCAGTTTGGAGACACAGGAAA 288
 QY 181 GTATCCCCAAATTCGAGATTATC 204
 DB 289 GTATCCCCAAATTCGAGATTATC 312

RESULT 6
 ABK93875
 ID ABK93875 standard; cDNA; 3000 BP.
 XX AC ABK93875;
 XX 26-AUG-2002 (first entry)
 DT Human cDNA encoding inhibitor of apoptosis, XIAP #2.
 DE Human; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX Homo sapiens.
 OS WO200226968-A2.
 PN 04-APR-2002.
 PD 27-SEP-2001; 2001WO-CA01379.
 XX 28-SEP-2000; 2000US-0672717.
 PR (UYOT-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 PI WPI; 2002-479562/51.
 DR Novel antisense inhibitor of apoptosis nucleic acid useful for
 PT enhancing apoptosis in a cell, for treating cancer and other
 PT proliferative diseases -
 XX Example 2; Fig 15; 135pp; English.
 XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC cDNA sequence.
 XX Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 other;
 SQ
 Query Match 100.0%; Score 204; DB 24; Length 3000;
 Best Local Similarity 100.0%; Pred. No. 1.1e-57;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAGTTTAATAGATTAAACACTTTTCTATATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 60
 DB 765 GAGTTTAATAGATTAAACACTTTTCTATATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 824
 QY 61 ACACCTGGCAGCAGCGGGTTTCTTATCTGTTGAAGAGATACCGTGGGTCTTTAGT 120
 DB 825 ACACCTGGCAGCAGCGGGTTTCTTATCTGTTGAAGAGATACCGTGGGTCTTTAGT 884

QY 121 TGTATGAGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
 DB 885 TGTATGAGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 944

QY 181 GTATCCCAAAATTCAGATTATC 204
 DB 945 GTATCCCAAAATTCAGATTATC 968

RESULT 7
 AAV55038
 ID AAV55038 standard; cDNA; 5232 BP.
 XX AC AAV55038;
 XX 13-NOV-1998 (first entry)
 DT
 DE Human XIAP coding sequence.
 XX
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX CDS 34..1527
 XX FT /*tag= a
 XX FT /product= XIAP

PN WO9835693-A2.
 XX 20-AUG-1998.
 XX 13-FEB-1998; 98WO-IB00781.
 XX 13-FEB-1997; 97US-0800929.
 XX (UYOT-) UNIV OTTAWA.
 XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
 XX Tsang B;
 XX WPI; 1998-467164/40.
 XX P-PSDB; AAW69294.
 XX Inducing apoptosis in proliferative mammalian cells with inhibitor
 XX of IAP or NAIP polypeptide - also methods for prognosis based on
 XX presence of IAP and NAIP, specifically applied to cancers involving
 XX p53 mutations
 XX
 XX Claim 13; Fig 1; 147pp; English.
 XX
 XX This sequence encodes the human XIAP protein, which is an inhibitor of
 XX apoptosis protein (IAP), and can be used in the method of the invention.
 XX The method is for enhancing apoptosis in cells from a mammal with
 XX proliferative disease by treatment with a compound that inhibits
 XX biological activity of an IAP or NAIP polypeptide. The inhibitory
 XX compounds are used to treat proliferative diseases, specially cancers of
 XX ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 XX liver nasopharynx, thyroid, central nervous system, prostate, colon,
 XX rectum, cervix or endometrium, particularly to increase their sensitivity
 XX to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 XX detected in many cancers and are associated with poor prognosis.
 XX resistance to chemotherapeutic agents and mutations in p53 (it is
 XX suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 XX genes). Transgenic animals are used for testing the effects of antisense
 XX oligonucleotides and for screening for the inhibitors.

QY Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;
 XX Query Match 100.0%; Score 204; DB 19; Length 5232;
 XX Best Local Similarity 100.0%; Pred. No. 1.4e-57;
 XX Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAAATAGATTAAAAAATTTTGGCTAATTTTCCAACTGCTAGTCTGTTTCAGCATCA 60
 DB 109 GAGTTTAAATAGATTAAAAAATTTTGGCTAATTTTCCAACTGCTAGTCTGTTTCAGCATCA 168

QY 61 AACTGGCAGCAGCAGGCTTTTCTTATATCTGTTGAAGAGATACCGTCCGCTGCTTTAGT 120
 DB 169 AACTGGCAGCAGCAGGCTTTTCTTATATCTGTTGAAGAGATACCGTCCGCTGCTTTAGT 228

QY 121 TGTATGCTCAGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
 DB 229 TGTATGCTCAGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 288

QY 181 GTATCCCAAAATTCAGATTATC 204
 DB 289 GTATCCCAAAATTCAGATTATC 312

RESULT 8
 AAT70839
 ID AAT70839 standard; cDNA; 2100 BP.
 XX AC AAT70839;
 XX 02-SEP-1997 (first entry)
 DT
 DE Mouse apoptosis inhibitor m-xiap cDNA.
 XX
 KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
 KW M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;
 KW ischaemia; myocardial infarction; stroke;
 KW reperfusion injury; toxin-induced liver disease; gene therapy;
 KW diagnosis; ds.
 XX
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 XX FH 127..1617
 XX CDS /*tag= . a
 XX FT
 XX WO9706255-A2.
 XX 20-FEB-1997.
 XX 05-AUG-1996; 96WO-IB01022.
 XX 22-DEC-1995; 95US-0576956.
 XX 04-AUG-1995; 95US-0511485.
 XX (UYOT-) UNIV OTTAWA.
 XX Baird S, Korneluk RG, Liston P, Mackenzie AE;
 XX WPI; 1997-154262/14.
 XX P-PSDB; AAW19584.
 XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
 XX to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
 XX of susceptibility to apoptotic disease
 XX
 XX Claim 11; Page 78-79; 219pp; English.
 XX Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and
 XX hiap-2 genes (AAW70836-41) respectively code for a new class of
 XX mammalian proteins (AAW19581-86) that are inhibitors of apoptosis
 XX (IAP). The murine xiap gene (for X-linked IAP gene) sequence was
 XX constructed from 12 overlapping clones isolated from a mouse
 XX embryo lambda-gt11 cDNA library and from a mouse Fix II genomic
 XX library using human xiap cDNA as probe. IAP nucleic acids can be
 XX used to express IAP polypeptides in cells and animals to inhibit
 XX apoptosis, and as primers and probes to identify and isolate
 XX additional IAP genes, as well as in methods for treating diseases
 XX and disorders involving apoptosis (anti-apoptotic gene therapy).

XX SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;

Query Match 84.3%; Score 172; DB 18; Length 2100;
 Best Local Similarity 90.2%; Pred. No. 4.6e-47;
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCCAAGTGGTAGCTGTTTCAGCATCA 60
 DB 202 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCCAAGTGGTAGCTGTTTCAGCATCA 261

QY 61 ACATGGCAGCAGCAGGCTTCTTATCTAGTGAAGAGATACCGTGGCTGCTTTAGT 120
 DB 262 ACATGGCAGCAGCAGGCTTCTTATCTAGTGAAGAGATACCGTGGCTGCTTTAGT 321

QY 121 TGTCATGAGCTGTAGATAGATGGAATATGAGACTCAGCAGTGGAGACACAGGAAA 180
 DB 322 TGTCATGAGCTGTAGATAGATGGAATATGAGACTCAGCAGTGGAGACACAGGAGA 381

QY 181 GTATCCCAAAATTCAGATTATC 204
 DB 382 ATATCCCAAAATTCAGATTATC 405

RESULT 9
 ABK93872
 ID ABK93872 standard; cDNA; 2100 BP.
 AC ABK93872;
 DT 26-AUG-2002 (first entry)
 DE Mouse cDNA encoding inhibitor of apoptosis, XIAP.
 KW Mouse; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytotatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX Mus sp.
 OS
 PN WO200226968-A2.
 XX
 XX PD 04-APR-2002.
 XX
 XX PF 27-SEP-2001; 2001WO-CA01379.
 XX
 XX PR 28-SEP-2000; 2000US-0672717.
 XX
 XX PA (UYOT-) UNIV OTTAWA.
 XX (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 XX PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX
 XX DR WPI: 2002-479562/51.
 XX P-PSDB; ABG65666.
 XX
 XX PT Novel antisense inhibitor of apoptosis nucleic acid useful for
 XX enhancing apoptosis in a cell, for treating cancer and other
 XX proliferative diseases
 XX
 XX PS Disclosure: Fig 4; 135pp; English.
 XX
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a

CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
 CC cDNA sequence.
 XX
 SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;

Query Match 84.3%; Score 172; DB 24; Length 2100;
 Best Local Similarity 90.2%; Pred. No. 4.6e-47;
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCCAAGTGGTAGCTGTTTCAGCATCA 60
 DB 202 GAGTTTAATAGATTAAACATTTTCTTAATTTTCCCAAGTGGTAGCTGTTTCAGCATCA 261

QY 61 ACATGGCAGCAGCAGGCTTCTTATCTAGTGAAGAGATACCGTGGCTGCTTTAGT 120
 DB 262 ACATGGCAGCAGCAGGCTTCTTATCTAGTGAAGAGATACCGTGGCTGCTTTAGT 321

QY 121 TGTCATGAGCTGTAGATAGATGGAATATGAGACTCAGCAGTGGAGACACAGGAAA 180
 DB 322 TGTCATGAGCTGTAGATAGATGGAATATGAGACTCAGCAGTGGAGACACAGGAGA 381

QY 181 GTATCCCAAAATTCAGATTATC 204
 DB 382 ATATCCCAAAATTCAGATTATC 405

RESULT 10
 AAV55041
 ID AAV55041 standard; cDNA; 2691 BP.
 XX
 AC AAV55041;
 XX
 XX DT 13-NOV-1998 (first entry)
 XX
 XX DE Murine XIAP coding sequence.
 XX
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.
 XX
 OS Mus sp.
 XX
 XX FH Key Location/Qualifiers
 XX CDS 672..2162
 XX FT /*tag= a
 XX FT /product= XIAP
 XX
 XX PN WO9835693-A2.
 XX
 XX PD 20-AUG-1998.
 XX
 XX PF 13-FEB-1998; 98WO-IB00781.
 XX
 XX PR 13-FEB-1997; 97US-0800929.
 XX
 XX PA (UYOT-) UNIV OTTAWA.
 XX
 XX PI Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
 XX Tsang B;
 XX
 XX DR WPI: 1998-467164/40.
 XX P-PSDB; AAW69297.
 XX
 XX PT Inducing apoptosis in proliferative mammalian cells with inhibitor
 XX of IAP or NAIP polypeptide - also methods for prognosis based on
 XX presence of IAP and NAIP, specifically applied to cancers involving


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PA (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-017444/02.
XX Chemically modified sequences of genes associated with apoptosis are
PT useful to determine methylation patterns of genomic DNA samples for
PT diagnosis of associated diseases such as cancer
XX claim 1; Seq ID #7; 24pp; English.
XX This invention relates to chemically pre-treated DNA of genes
CC associated with apoptosis. The nucleic acids are used to allocate
CC patients for specific therapy for HIV infection, Bloom syndrome, virus
CC cardiopathy, aging, neurodegenerative disorders, Herpes simplex, virus
CC infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours
CC and cancers. This nucleotide sequence represents a chemically
CC treated apoptosis gene. Even SEQ ID numbers are the complementary
CC DNA strands to the odd SEQ ID numbers. The sequence data for this
CC patent is not represented in the printed specification but is based on
CC information supplied by the European patent office.
XX
SQ Sequence 7990 BP; 2223 A; 102 C; 1567 G; 4098 T; 0 other;

Query Match 75.2%; Score 153.4; DB 24; Length 7990;
Best Local Similarity 84.7%; Pred. No. 1.4e-40;
Matches 172; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 GAGTTAATAGATTAAACCTTTCTTAATTTTCCAAGTGTAGTCCTGTTTCAGCATCA 60
DB 5109 GAGTTAATAGATTAAACCTTTCTTAATTTTCCAAGTGTAGTCCTGTTTCAGCATCA 60
QY 61 ACACCTGGCAGCAGCGGTTCTTTATCTGCTGAAGGAGATACGTCGGTCTTACT 120
DB 5169 ATATTGGTACGAGTAGGGTTTTTATATGTTGTAAGGAGATATCGTCGGTCTTACT 528
QY 121 TGTCAATGACGCTGTAGATAGATGCAATATGAGACTCAGCAGTTGGAAGACACAGGAAA 180
DB 5229 TGTATGATGTTGTAGATAGATGGAATATGAGATTTAGTAGTTGGAAGATATAGGAAA 5288
QY 181 GTATCCCAAAATTCAGATTTAT 203
DB 5289 GTATTTTAAATTTAGATTTAT 5311

RESULT 13
ABL32158
ID ABL32158 standard; DNA; 7990 BP.
XX ABL32158;
XX
DT 26-MAR-2002 (first entry)
XX
DE Human immune system associated gene SEQ ID NO: 131.
XX
KW Human; immune system disease; cytosine methylation; antiasthmatic;
KW antiarteriosclerotic; antianaemic; cytosinostatic; nootropic;
KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
KW gene; ds.
XX
OS Homo sapiens.
XX
PN WO200200928-A2.
XX
XX 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.
XX

PR 30-JUN-2000; 2000DE-1032529.
PR 01-SEP-2000; 2000DE-1043826.
XX (EPIG-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K;
XX WPI; 2002-130909/17.
XX Nucleic acid comprising fragment of chemically modified gene, useful
PT for diagnosis and treatment of diseases associated with abnormal
PT cytosine methylation
XX
XX Claim 1; SEQ ID NO 131; 32pp + Sequence Listing; German.
XX The present invention provides a number of human immune system associated
CC genes which are modified by the methylation of cytosines. The sequences
CC can be used in the diagnosis and treatment of immune system disorders,
CC including eye diseases such as retinopathy, neovascular glaucoma and
CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
CC diseases. The present sequence is a gene of the invention.
XX
SQ Sequence 7990 BP; 2223 A; 102 C; 1567 G; 4098 T; 0 other;

Query Match 75.2%; Score 153.4; DB 24; Length 7990;
Best Local Similarity 84.7%; Pred. No. 1.4e-40;
Matches 172; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 1 GAGTTAATAGATTAAACCTTTCTTAATTTTCCAAGTGTAGTCCTGTTTCAGCATCA 60
DB 5109 GAGTTAATAGATTAAACCTTTCTTAATTTTCCAAGTGTAGTCCTGTTTCAGCATCA 60
QY 61 ACACCTGGCAGCAGCGGTTCTTTATCTGCTGAAGGAGATACGTCGGTCTTACT 120
DB 5169 ATATTGGTACGAGTAGGGTTTTTATATGTTGTAAGGAGATATCGTCGGTCTTACT 528
QY 121 TGTCAATGACGCTGTAGATAGATGCAATATGAGACTCAGCAGTTGGAAGACACAGGAAA 180
DB 5229 TGTATGATGTTGTAGATAGATGGAATATGAGATTTAGTAGTTGGAAGATATAGGAAA 5288
QY 181 GTATCCCAAAATTCAGATTTAT 203
DB 5289 GTATTTTAAATTTAGATTTAT 5311

RESULT 14
ABL54308/C
ID ABL54308 standard; DNA; 7990 BP.
XX ABL54308;
XX
DT 29-JUL-2002 (first entry)
XX
DE Chemically treated apoptosis gene complementary to gene #4.
XX
KW Apoptosis; HIV; Bloom syndrome; cardiopathy;
KW neurodegenerative disorder; Herpes simplex virus; renal ischaemia;
KW amyotrophic lateral sclerosis; cancer; ds.
XX
OS Unidentified.
XX
PN WO200177164-A2.
XX
XX 18-OCT-2001.
XX
XX 06-APR-2001; 2001WO-EP03969.
XX
XX 06-APR-2000; 2000DE-1019058.
XX 07-APR-2000; 2000DE-1019173.
XX 30-JUN-2000; 2000DE-1032529.
XX 01-SEP-2000; 2000DE-1043826.
XX

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XX	(EPIG-) EPIGENOMICS AG.
XX	Olek A, Piepenbrock C, Berlin K;
XX	WPI; 2002-017444/02.
XX	Chemically modified sequences of genes associated with apoptosis are
PT	used to determine methylation patterns of genomic DNA samples for
PT	diagnosis of associated diseases such as cancer -
XX	Claim 1, Seq ID #8; 24pp; English.
XX	This invention relates to chemically pre-treated DNA of genes
CC	associated with apoptosis. The nucleic acids are used to allocate
CC	patients for specific therapy for HIV infection, Bloom syndrome,
CC	cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus
CC	infection, renal ischemia, amyotrophic lateral sclerosis, solid tumours
CC	and cancers. This nucleotide sequence represents a chemically
CC	treated apoptosis gene. Even SEQ ID numbers are the complementary
CC	DNA strands to the odd SEQ ID numbers. The sequence data for this
CC	patent is not represented in the printed specification but is based on
CC	information supplied by the European patent office.
XX	Sequence 7990 BP; 2539 A; 102 C; 1661 G; 3688 T; 0 other;
SQL	Query Match 63.4%; Score 129.4; DB 24; Length 7990;
	Best Local Similarity 77.3%; Pred. No. 1.e-32;
	Matches 157; Conservative 0; Mismatches 46; Indels 0; Gaps 0;
QY	2 AGTTATAGATTAAAACTTTTGCTAATTTTCCAAGTGGTAGTCCTGTTTCAGCATCAA 61
Db	2881 AATTTATAAATTAAACATTTTACTAATTTTCAAAATAATAATCCTATTTC AACATCAA 2822
QY	62 CACTGGCACAGCAGGGTTCTTTTATCTGTGTGAAGGAGATACCGTGGCGGCTTTAGTT 121
Db	2821 CACTAACACGCAACAAAATTTCTTTTATACTATAAAAAAATACCCTACGATCACTTTAAT 2762
QY	122 GTCATGCAGGTGTAGATGATGGCAATATGGAGACTTCAGCAGTTTGGAAAGACACAGGAAAG 181
Db	2761 ATCATACAACATTAATAATAACATATAAAACTCAACAATTA AAAACACAA AAAA 2702
QY	182 TATCCCCAAATTTGCAGATTTATC 204
Db	2701 TATCCCCAAATTTACAAATTTATC 2679

RESULT 15

RESULT 13
ABL32159/c
ID ABL32159 standard: DNA: 7990 BP.

AC ABL32159:

XX
XX
XXXXXXX

SECRET

DT 26-MAR-2002 (first entry)

XX
DE
Human immune system associated gene SEQ ID NO: 132.

KW Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; anianaemic; cyostatic; nootropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antirheumatic; antiarthritic; antidabetic; antipsoriatic;
 KW antinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KW gene: ds.

OS Homo sapiens.

PN WO200200928-A2.

[illegible]

PD 03-JAN-2002.
XX
PF 02-JUL-2001; 2001WO-EP07537.

	XX	30-JUN-2000; 2000DB-1032529.	
	PR	01-SEP-2000; 2000DE-1043826.	
	XX	(EPIG-) EPIGENOMICS AG.	
	XX	Olek A, Piepenbrock C, Berlin K;	
	XX	WPI; 2002-130909/17.	
	DR	Nucleic acid comprising fragment of chemically modified gene, useful for diagnosis and treatment of diseases associated with abnormal cytosine methylation	
	PT		
	PT		
	PS	Claim 1; SEQ ID NO 132; 32pp + Sequence Listing; German.	
	XX	The present invention provides a number of human immune system associated genes which are modified by the methylation of cytosines. The sequences can be used in the diagnosis and treatment of immune system disorders, including eye diseases such as retinopathy, neovascular glaucoma and macular degeneration, arteriosclerosis, anemia, cancer, acute myeloid leukemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis, rheumatoid arthritis, psoriasis and inflammatory ulcerative bowel diseases. The present sequence is a gene of the invention.	
	XX	Sequence 7990 BP; 2539 A; 102 C; 1661 G; 3688 T; 0 other;	
	SQ	Query Match 63.4%; Score 129.4; DB 24; Best Local Similarity 77.3%; Pred. No. 1.4e-32; Matches 157; Conservative 0; Mismatches 46; Indels 0; Gaps 0;	
	Qy	2 AGTTTATAGATTAAACACTTTTGCTAATTTTCGAATGGTAGTCCGTTTCAGCATCAA 61	
	Db	 2881 AA TT TA AT AAA ACT TT TTA CT AAT TT TC CA AA ATAATAA CT ATT TCA CATCAA 2822	
	Qy	62 CACTGGCAGCACGCGGTTCCTTTATCTGC GTGAGGAGATACC GG CGGTGCTTTAGTT 121	
	Db	 2821 CAC TA AC CAC GA CA AAAAA TTCCTTTATACA TAAA AAAAA ACC GCAGTACTTTAAT 2762	
	Qy	122 GTA TG CAG CTC GTG TAG ATAG TGG CA ATATGG AGACTCAG CAGT TGG AAGA CAC AGCAAG 181	
	Db	 2761 ATC ATAC AAC TTAATAAATAAACATATAAAACTCA ACAATTAAAAA ACACA AAAAAA 2702	
	Qy	182 TATCCCCAAATTCGAGATTTATC 204	
	Db	 2701 TATCCC AAAAT TACA AAAATTTATC 2679	

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OM nucleic - nucleic search, using sw model

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Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 852724

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	204	100.0	1588	4	US-09-239-867-3 Sequence 3, Appli
2	204	100.0	2540	2	US-08-511-485-3 Sequence 3, Appli
3	204	100.0	2540	3	US-09-392-580-1 Sequence 1, Appli
4	204	100.0	5232	3	US-09-212-971-3 Sequence 3, Appli
5	204	100.0	5232	3	US-08-800-929A-3 Sequence 3, Appli
6	204	100.0	5232	4	US-09-617-053A-3 Sequence 3, Appli
7	172	84.3	2100	2	US-08-511-485-9 Sequence 9, Appli
8	172	84.3	2691	3	US-09-212-971-9 Sequence 9, Appli
9	172	84.3	2691	3	US-08-800-929A-9 Sequence 9, Appli
10	172	84.3	2691	4	US-09-617-053A-9 Sequence 9, Appli
11	68.4	33.5	1559	4	US-09-239-867-1 Sequence 1, Appli
12	62.2	30.5	2676	3	US-09-212-971-11 Sequence 11, Appli
13	62.2	30.5	2676	3	US-08-800-929A-11 Sequence 11, Appli
14	62.2	30.5	2676	4	US-09-617-053A-11 Sequence 11, Appli
15	62.2	30.5	2862	4	US-08-569-749-13 Sequence 13, Appli
16	62.2	30.5	2862	5	PCT-US96-12860-13 Sequence 13, Appli
17	62.2	30.5	3151	3	US-09-212-971-13 Sequence 13, Appli
18	62.2	30.5	3151	3	US-08-800-929A-13 Sequence 13, Appli
19	62.2	30.5	3151	4	US-09-617-053A-13 Sequence 13, Appli
20	56	27.5	2676	2	US-08-511-485-5 Sequence 5, Appli
21	56	27.5	3076	2	US-09-205-144-1 Sequence 1, Appli
22	56	27.5	6669	3	US-09-212-971-5 Sequence 5, Appli
23	56	27.5	6669	3	US-08-800-929A-5 Sequence 5, Appli
24	56	27.5	6669	4	US-09-617-053A-5 Sequence 5, Appli
25	55.8	27.4	2580	2	US-08-511-485-7 Sequence 7, Appli
26	55.8	27.4	2589	4	US-08-569-749-1 Sequence 1, Appli
27	55.8	27.4	2589	5	PCT-US96-12860-1 Sequence 1, Appli

28	55.8	27.4	3532	2	US-09-205-204-1 Sequence 1, Appli
29	55.8	27.4	3732	3	US-09-212-971-7 Sequence 7, Appli
30	55.8	27.4	3732	3	US-08-800-929A-7 Sequence 7, Appli
31	55.8	27.4	3732	4	US-09-617-053A-7 Sequence 7, Appli
32	54.4	26.7	2601	4	US-08-569-749-3 Sequence 3, Appli
33	54.4	26.7	2601	5	PCT-US96-12860-3 Sequence 3, Appli
34	52.2	25.6	5502	3	US-08-836-134-1 Sequence 1, Appli
35	52.2	25.6	5502	4	US-09-493-784-1 Sequence 1, Appli
36	42.4	20.8	1435	5	PCT-US95-05922A-1 Sequence 1, Appli
37	34.4	16.9	711	3	US-09-121-979-3 Sequence 3, Appli
38	34.4	16.9	711	4	US-09-332-319-3 Sequence 3, Appli
39	31.4	15.4	374	4	US-09-328-111-423 Sequence 423, App
40	30.8	15.1	176373	3	US-09-128-155-17 Sequence 17, Appli
c 41	30.4	14.9	1725	4	US-09-062-440-1 Sequence 1, Appli
c 42	30.4	14.9	1725	4	US-09-712-495-1 Sequence 1, Appli
43	29	14.2	2556	3	US-08-699-103B-9 Sequence 9, Appli
44	29	14.2	2556	4	US-09-229-059-9 Sequence 9, Appli
45	29	14.2	2731	3	US-08-699-103B-11 Sequence 11, Appli

ALIGNMENTS

RESULT 1
US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-239-867-3

Query Match	100.0%	Score 204:	DB 4:	Length 1588:
Best Local Similarity	100.0%	Pred. No. 1.1e-55:		
Matches 204;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY 1	GAGTTTAATAGATTAAAACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60			
Db 109	GAGTTTAATAGATTAAAACTTTTGTCTAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 168			
QY 61	ACACTGGCAGCAGCAGGGTTCTTTTATCTAGTGAAGGAGATACCGTGGGTGCTTTAGT 120			
Db 169	ACACTGGCAGCAGCAGGGTTCTTTTATCTAGTGAAGGAGATACCGTGGGTGCTTTAGT 228			
QY 121	TGTCATGACGCTAGATAGATGGCAATATGAGACTCAGCAGTGGGAAGACACAGGAAA 180			
Db 229	TGTCATGACGCTAGATAGATGGCAATATGAGACTCAGCAGTGGGAAGACACAGGAAA 288			
QY 181	GTATCCCAAAATTCAGATTATC 204			
Db 289	GTATCCCAAAATTCAGATTATC 312			

RESULT 2
US-08-511-485-3
; Sequence 3, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen

;; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
;; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
;; NUMBER OF SEQUENCES: 38
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/511,485
;; FILING DATE: 04-AUG-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T.
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 07540/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2540 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: DNA (genomic)
US-08-511-485-3

Query Match 100.0%; Score 204; DB 2; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.4e-55;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
|||||
Db 109 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 168
QY 61 ACACCTGGCAGCAGCAGGGTTCTTTATCTGTGTGAAGGAGATACCGTGGGTGCTTTAGT 120
|||||
Db 169 ACACCTGGCAGCAGCAGGGTTCTTTATCTGTGTGAAGGAGATACCGTGGGTGCTTTAGT 228
QY 121 TGTCTATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
|||||
Db 229 TGTCTATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 288
QY 181 GTATCCCAAAATTCAGATTATC 204
|||||
Db 289 GTATCCCAAAATTCAGATTATC 312

RESULT 3
US-09-392-580-1
;; Sequence 1, Application US/09392580
;; Patent No. 6087173
;; GENERAL INFORMATION:
;; APPLICANT: C. Frank Bennett
;; APPLICANT: Elizabeth J. Ackermann
;; APPLICANT: Lex M. Cowsert
;; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION
;; FILE REFERENCE: RTS-0072
;; CURRENT APPLICATION NUMBER: US/09/392,580
;; CURRENT FILING DATE: 1999-09-09
;; NUMBER OF SEQ ID NOS: 47
;; SEQ ID NO 1
;; LENGTH: 2540
;; TYPE: DNA

;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (34)...(1527)
US-09-392-580-1

Query Match 100.0%; Score 204; DB 3; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.4e-55;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
|||||
Db 109 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 168
QY 61 ACACCTGGCAGCAGCAGGGTTCTTTATCTGTGTGAAGGAGATACCGTGGGTGCTTTAGT 120
|||||
Db 169 ACACCTGGCAGCAGCAGGGTTCTTTATCTGTGTGAAGGAGATACCGTGGGTGCTTTAGT 228
QY 121 TGTCTATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
|||||
Db 229 TGTCTATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 288
QY 181 GTATCCCAAAATTCAGATTATC 204
|||||
Db 289 GTATCCCAAAATTCAGATTATC 312

RESULT 4

US-09-212-971-3
;; Sequence 3, Application US/09212971B
;; Patent No. 6107041
;; GENERAL INFORMATION:
;; APPLICANT: Korneluk, Robert G
;; APPLICANT: Mackenzie, Alexander E
;; APPLICANT: Liston, Peter
;; APPLICANT: Baird, Stephen
;; APPLICANT: Tsang, Benjamin K
;; APPLICANT: Pratt, Christine
;; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;; TITLE OF INVENTION: DISEASE
;; FILE REFERENCE: 07891/009002
;; CURRENT APPLICATION NUMBER: US/09/212,971B
;; CURRENT FILING DATE: 1998-12-16
;; EARLIER APPLICATION NUMBER: 60/017,354
;; EARLIER FILING DATE: 1996-04-26
;; EARLIER APPLICATION NUMBER: 60/030,590
;; EARLIER FILING DATE: 1996-11-14
;; EARLIER APPLICATION NUMBER: 08/800,929
;; EARLIER FILING DATE: 1997-02-13
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 3
;; LENGTH: 5232
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: variation
;; LOCATION: (4623)...(4623)
;; OTHER INFORMATION: n can be any nucleotide
;; FEATURE:
;; NAME/KEY: variation
;; LOCATION: (4622)...(4622)
;; OTHER INFORMATION: n can be any nucleotide
US-09-212-971-3

Query Match 100.0%; Score 204; DB 3; Length 5232;
Best Local Similarity 100.0%; Pred. No. 1.8e-55;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
|||||
Db 109 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 168

Db	109	GAGTTTATAGATTAAAACTTTGCTAATTTCCAGTGGTAGCTGTTTCAGCATCA	168
Qy	61	ACACTGGCACGAGCAGGGTTCTTTATCTGGTGAAGGAGATACCGTGGGGTGCTTTAGT	120
Db	169	ACACTGGCACGAGCAGGGTTCTTTATCTGGTGAAGGAGATACCGTGGGGTGCTTTAGT	228
Qy	121	TGTCATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTTGGAGACACAGGAAA	180
Db	229	TGTCATGCAGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTTTGGAGACACAGGAAA	288
Qy	181	GTATCCCAAAATTGCAGATTTATC	204
Db	289	GTATCCCAAAATTGCAGATTTATC	312

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RESULT 7
US-08-511-485-9
; Sequence 9, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511.485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match      84.3%; Score 172; DB 2; Length 2100;
Best Local Similarity 90.2%; Pred. No. 1.9e-45;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCCAAGTGGTAGTCCTGTTTCAGCATCA 60
    |||||||
DB 202 GAGTTTAATAGATTAAACACTTTTCTTAATTTCCCAAGTGGTAGTCCTGTTTCAGCATCA 261
    |||||||

QY 61 ACACGTGGCAGCAGAGGGTTCCTTTATCTGTTGAAGAGATACCGTGGCGGCTTTTACT 120
    |||||||
DB 262 ACATTTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTCAATGTTTCAGT 321
    |||||||

QY 121 TGTCTATGAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTGGAGACACAGGAAA 180
    |||||||
DB 322 TGTCTATGAGCTGTAGATAGATGGCAATATGAGACTCAGCAGTGGAGACACAGGAGA 381
    |||||||

QY 181 GTATCCCAAAATTGCAGATTATC 204
    |||||||
DB 382 ATATCCCAAAATTGCAGATTATC 405
    |||||||

RESULT 8
US-09-212-971-9
; Sequence 9, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
```

; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2691 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-800-929A-9

Query Match 84.3%; Score 172; DB 3; Length 2691;
Best Local Similarity 90.2%; Pred. No. 2.le-45;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 GAGTTTAAATAGATTAAAAACCTTTTGCCTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCA 60
DB 747 GAGTTTAAATAGATTAAAAACCTTTTGCCTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCA 806
QY 61 ACATGGCAGCAGGAGGTTTCTTTATACCTGGTGAAGAGAGATACCGTGGTGTCTTTAGT 120
DB 807 ACATTGGCGGAGCTGGTGTCTTTATACCGGTGAAGAGAGACACCGTGCATGTTTCAGT 866
QY 121 TGTATGCTGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
DB 867 TGTATGCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTTGAAGACACAGGAGA 926
QY 181 GTATCCCCAAATTCAGATTATC 204
DB 927 ATATCCCCAAATTCAGATTATC 950

RESULT 10
US-09-617-053A-9
; Sequence 9, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-617-053A-9

Query Match 84.3%; Score 172; DB 4; Length 2691;
Best Local Similarity 90.2%; Pred. No. 2.le-45;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 GAGTTTAAATAGATTAAAAACCTTTTGCCTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCA 60
DB 747 GAGTTTAAATAGATTAAAAACCTTTTGCCTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCA 806
QY 61 ACATGGCAGCAGGAGGTTTCTTTATACCTGGTGAAGAGAGATACCGTGGTGTCTTTAGT 120
DB 807 ACATTGGCGGAGCTGGTGTCTTTATACCGGTGAAGAGAGACACCGTGCATGTTTCAGT 866
QY 121 TGTATGCTGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
DB 867 TGTATGCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTTGAAGACACAGGAGA 926
QY 181 GTATCCCCAAATTCAGATTATC 204
DB 927 ATATCCCCAAATTCAGATTATC 950

RESULT 11
US-09-239-867-1
; Sequence 1, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1559
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: (1)-(1559)
; OTHER INFORMATION: n = A,T,C or G
US-09-239-867-1

Query Match 33.5%; Score 68.4; DB 4; Length 1559;
Best Local Similarity 64.7%; Pred. No. 1.6e-12;
Matches 132; Conservative 0; Mismatches 46; Indels 26; Gaps 1;
QY 1 GAGTTTAAATAGATTAAAAACCTTTTGCCTAATTTTCCAAAGTGTAGTCCCTGTTTCAGCATCA 60
DB 109 GAGATTAAATAGATTAAAAACCTTTTGCCTGCTTTGAGGTGGTGGCTGCTGGGCGCATCG 168
QY 61 ACATGGCAGCAGGAGGTTTCTTTATACCTGGTGAAGAGAGATACCGTGGTGTCTTTAGT 120
DB 169 GGC-----GTTGAGGAGAGACGCTGGGGGGGCTTAGC 202
QY 121 TGTATGCTGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
DB 203 TCCCTGAGCGGTAGACAGGTGGCAACGCTGGGGCTCAGGAGTTGACAAACACACAGAAA 262
QY 181 GTATCCCCAAATTCAGATTATC 204
DB 263 GCAGGCGCGAATTCAGATTATC 286

RESULT 12
US-09-212-971-11
; Sequence 11, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G

APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2676
TYPE: DNA
ORGANISM: Mus musculus
US-09-212-971-11

Query Match 30.5%; Score 62.2; DB 3; Length 2676;
Best Local Similarity 56.7%; Pred. No. 1.8e-10;
Matches 115; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 1 GAGTTTATAGATTAAACCTTTCTTAATTTTCCAACTGGTAGTCTGCTTTTCCAGCATCA 60
DB 381 GAGCTGTACCGATTGTCACGATTTCAGCTTTTCCAGGGAGTCTGCTGTCAGAAAGG 440
QY 61 ACATCGGCACGACGAGGCTTTCTTTATCTGTTGAAGGAGATACCGTGGGTCCTTTAGT 120
DB 441 AGTCTGGCTGCTGCTGGCTTTTACTACACTGTGTCCTGCAAGGTCAAGTCTCTGTC 500
QY 121 TGTCATGACGTGTAGTAGATGATGCAATATGAGACTCAGAGTTGGAAGACACAGGAAA 180
DB 501 TGTGCGCTGTAGTACACACTGGAACAGGGGACACTCCATGAGGAGACACAGAAAG 560
QY 181 GTATCCCAAAATTCAGATTAT 203
DB 561 TTGTACCCCGAGTGCACACTTGT 583

RESULT 13
US-08-800-929A-11
Sequence 11, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
NAME: Bleker-Brady, Kristina
ATTORNEY/AGENT INFORMATION:
REGISTRATION NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 2676 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-800-929A-11

Query Match 30.5%; Score 62.2; DB 3; Length 2676;
Best Local Similarity 56.7%; Pred. No. 1.8e-10;
Matches 115; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 1 GAGTTTATAGATTAAACCTTTCTTAATTTTCCAACTGGTAGTCTGCTTTTCCAGCATCA 60
DB 381 GAGCTGTACCGATTGTCACGATTTCAGCTTTTCCAGGGAGTCTGCTGTCAGAAAGG 440
QY 61 ACATCGGCACGACGAGGCTTTCTTTATCTGTTGAAGGAGATACCGTGGGTCCTTTAGT 120
DB 441 AGTCTGGCTGCTGCTGGCTTTTACTACACTGTGTCCTGCAAGGTCAAGTCTCTGTC 500
QY 121 TGTCATGACGTGTAGTAGATGATGCAATATGAGACTCAGAGTTGGAAGACACAGGAAA 180
DB 501 TGTGCGCTGTAGTACACACTGGAACAGGGGACACTCCATGAGGAGACACAGAAAG 560
QY 181 GTATCCCAAAATTCAGATTAT 203
DB 561 TTGTACCCCGAGTGCACACTTGT 583

RESULT 14
US-09-617-053A-11
Sequence 11, Application US/09617053A
Patent No. 6300492
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US/08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 2676
TYPE: DNA
ORGANISM: Mus musculus
US-09-617-053A-11

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:33:02 ; Search time 49.0521 Seconds
(without alignments)
3648.005 Million cell updates/sec

Title: US-09-654-743-45

Perfect score: 204

Sequence: 1 gagtttaaatagattaaac.....ccccaaattgcagattatc 204

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186658

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:*
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	100.0	2404	9	US-09-964-899-38
2	204	100.0	2540	9	US-09-201-936-3
3	204	100.0	5232	10	US-09-974-592-3
4	172	84.3	2100	9	US-09-201-936-9
5	172	84.3	2691	10	US-09-974-592-9
6	62.2	30.5	2416	9	US-09-201-936-41
7	62.2	30.5	2450	9	US-09-201-936-39
8	62.2	30.5	2676	10	US-09-974-592-11
9	62.2	30.5	3151	10	US-09-974-592-13
10	56	27.5	2676	9	US-09-201-936-5
11	56	27.5	3076	9	US-09-954-531-16
12	56	27.5	3076	10	US-09-954-456-1635
13	56	27.5	6669	10	US-09-974-592-5
14	55.8	27.4	2580	9	US-09-201-936-7
15	55.8	27.4	3532	10	US-09-880-107-3354
16	55.8	27.4	3732	10	US-09-974-592-7
17	54.2	26.6	2291	10	US-09-778-927A-21
18	52.2	25.6	5504	8	US-08-913-322-1
19	52.2	25.6	6124	8	US-08-913-322-21

Sequence 184, App
Sequence 2, Appli
Sequence 23, Appl
Sequence 6687, Ap
Sequence 3493, Ap
Sequence 3213, Ap
Sequence 182, App
Sequence 423, App
Sequence 248, App
Sequence 17, Appl
Sequence 140, App
Sequence 51, Appl
Sequence 1598, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 125, App
Sequence 116, App
Sequence 291, App
Sequence 500, App
Sequence 500, App
Sequence 291, App
Sequence 500, App
Sequence 500, App
Sequence 291, App
Sequence 291, App
Sequence 291, App

20 52.2 25.6 6124 10 US-09-967-768A-184
21 52.2 25.6 6133 8 US-08-913-322-2
22 52.2 25.6 6228 8 US-08-913-322-23
23 41 20.1 240 9 US-09-796-692-6687
24 39.4 19.3 240 9 US-09-796-692-3493
25 31.4 15.4 285 9 US-09-796-692-3213
26 31.4 15.4 314 10 US-09-920-300A-182
27 31.4 15.4 314 12 US-10-033-528-182
28 31.4 15.4 374 10 US-09-879-536-423
29 31.4 15.4 571 12 US-10-044-090-248
30 30.8 15.1 176373 9 US-10-095-407-17
31 30.6 15.0 7992 9 US-08-893-519A-140
32 30.6 15.0 8493 9 US-10-071-766-51
33 30.4 14.9 1587 9 US-09-938-842A-1598
34 30.4 14.9 1725 9 US-10-075-074-1
35 29.8 14.6 11186 10 US-09-957-997-1
36 29.6 14.5 2193 10 US-09-801-368-125
37 29.6 14.5 2851 9 US-10-114-893-116
38 29.6 14.5 2906 9 US-09-905-291A-291
39 29.6 14.5 2906 9 US-09-982-598-500
40 29.6 14.5 2906 9 US-09-989-293A-500
41 29.6 14.5 2906 9 US-09-902-853-291
42 29.6 14.5 2906 9 US-09-989-735-500
43 29.6 14.5 2906 9 US-09-990-444-500
44 29.6 14.5 2906 9 US-09-907-824-291
45 29.6 14.5 2906 9 US-09-907-841-291

ALIGNMENTS

RESULT 1
US-09-964-899-38
; Sequence 38, Application US/09964899
; Patent NO. US2002017446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo Sapien
; US-09-964-899-38

Query Match 100.0%; Score 204; DB 9; Length 2404;
Best Local Similarity 100.0%; Pred. No. 2.5e-56;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGTTTAAATAGATTAAACCTTTTCTAATTTTCCAAGTGGTAGTCTCTTTTCAGCATCA 60
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DB 109 GAGTTTAAATAGATTAAACCTTTTCTAATTTTCCAAGTGGTAGTCTCTTTTCAGCATCA 168
QY 61 ACACCTGGCAGCAGCAGGGTTCCTTTTACTGTGTGAAGAGATACCGTGGCGGTCTTTTACT 120
|||||
DB 169 ACACCTGGCAGCAGCAGGGTTCCTTTTACTGTGTGAAGAGATACCGTGGCGGTCTTTTACT 228
QY 121 TGTCTATGACGCTGTAGATAGATGGCAATATGAGACTCAGCAGTGTGGAGACACAGGAAA 180
|||||
DB 229 TGTCTATGACGCTGTAGATAGATGGCAATATGAGACTCAGCAGTGTGGAGACACAGGAAA 288
QY 181 GTATCCCAAAATTCAGATTTTATC 204
|||||
DB 289 GTATCCCAAAATTCAGATTTTATC 312


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Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 GAGTTAATAGATTAATAAATCTTGGTAAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
Db 202 GAGTTAATAGATTAATAAATCTTGGTAAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 261
QY 61 ACACCTGGCAGCAGGAGGTTCTTTATACCTGGTGAAGGAGATACCGTGGTGGTCTTTAGT 120
Db 262 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGGCAATGTTTCAGT 321
QY 121 TGTCTATGCACGCTAGATAGATGGAATATGGAGACTCAGCTGTTGGAAGACACAGGAAA 180
Db 322 TGTCTATGCACGCTAGATAGATGGAATATGGAGACTCAGCTGTTGGAAGACACAGGAGA 381
QY 181 GTATCCCAAAATTCAGATTATC 204
Db 382 ATATCCCAAAATTCAGATTATC 405
RESULT 5
US-09-974-592-9
; Sequence 9, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; FILE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-974-592-9
Query Match 84.3%; Score 172; DB 10; Length 2691;
Best Local Similarity 90.2%; Pred. No. 7e-46;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 GAGTTAATAGATTAATAAATCTTGGTAAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
Db 747 GAGTTAATAGATTAATAAATCTTGGTAAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 806
QY 61 ACACCTGGCAGCAGGAGGTTCTTTATACCTGGTGAAGGAGATACCGTGGTGGTCTTTAGT 120
Db 807 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGGCAATGTTTCAGT 866
QY 121 TGTCTATGCACGCTAGATAGATGGAATATGGAGACTCAGCTGTTGGAAGACACAGGAAA 180
Db 867 TGTCTATGCACGCTAGATAGATGGAATATGGAGACTCAGCTGTTGGAAGACACAGGAGA 926
QY 181 GTATCCCAAAATTCAGATTATC 204
Db 927 ATATCCCAAAATTCAGATTATC 950
RESULT 6
US-09-201-936-41
; Sequence 41, Application US/09201936
; Publication No. US20020187946A1
```

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; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-41
Query Match 30.5%; Score 62.2; DB 9; Length 2416;
Best Local Similarity 56.7%; Pred. No. 3.8e-10;
Matches 115; Conservative 0; Mismatches 88; Indels 0; Gaps 0;
QY 1 GAGTTAATAGATTAATAAATCTTGGTAAATTTTCCAAAGTGGTAGTCTCTTTTCAGCATCA 60
Db 215 GAACCTTACCGAATGTCTACATATTCAGCTTTCCCAAGGAGTCTCTGTCTCAGAGG 274
QY 61 ACACCTGGCAGCAGGAGGTTCTTTATACCTGGTGAAGGAGATACCGTGGTGGTCTTTAGT 120
Db 275 AGCTGGCTGGTGGTCTTTTATACAGGTGTGAATGACAAAGTCAAGTGTCTCTGC 334
QY 121 TGTCTATGCACGCTAGATAGATGGAATATGGAGACTCAGCTGTTGGAAGACACAGGAAA 180
Db 335 TGTGGCTGTATGTTGGATACTGGAACAAAGGGGACAGTCTCTGTTGAAAGACACAGAG 394
QY 181 GTATCCCAAAATTCAGATTATC 203
Db 395 TTCTATCCCAAGTGCAGCTTGT 417
RESULT 7
US-09-201-936-39
; Sequence 39, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 39
; LENGTH: 2450
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EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 5
LENGTH: 2676
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (2470)...(2470)
OTHER INFORMATION: N may be any nucleotide
FEATURE:
NAME/KEY: variation
LOCATION: (2476)...(2476)
OTHER INFORMATION: N may be any nucleotide
FEATURE:
NAME/KEY: variation
LOCATION: (2483)...(2483)
OTHER INFORMATION: N may be any nucleotide
FEATURE:
NAME/KEY: variation
LOCATION: (2602)...(2602)
OTHER INFORMATION: N may be any nucleotide
US-09-201-936-5

Query Match 27.5%; Score 56; DB 9; Length 2676;
Best Local Similarity 55.0%; Pred. No. 4.2e-08;
Matches 110; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
Qy 1 GAGTTTAATAGATTAAACATTTTGGCTAATTTTCCAACTGGTAGTCCCTGTTTCAGCATCA 60
Db 273 GAACGTGTACCGAATGCTACGTAATCCACTTTTCTGCTGGGTTCCTGCTCAGAAAGG 332
Qy 61 ACACCTGGCAGCAGGAGGTTTCTTTATCTACTGGTGNAGAGATACCGTCCGGTGGCTTTAGT 120
Db 333 AGTCTTGCTGCTGGTGTCTTATACACTGGTGTGAATGACAGGTCAAAATGCTTCTGT 392
Qy 121 TGTCTATGACGTGTAGATAGATGGAATATGAGACTCAGCAGTGTGGAAGACACAGGAAA 180
Db 393 TGTGGCTGTAGTGGATACTGGAAAGAGAGAGACAGTCTTACTGAAAGCATATAAAG 452
Qy 181 GTATCCCCAAATTCAGATT 200
Db 453 TTGTATCCTAGTCAGATT 472

RESULT 11
US-09-954-531-16
Sequence 16, Application US/09954531
Patent No. US20020165180A1
GENERAL INFORMATION:
APPLICANT: Weaver, Zoe
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Candi
FILE REFERENCE: 689290-77
CURRENT APPLICATION NUMBER: US/09/954,531
CURRENT FILING DATE: 2002-05-02
PRIOR APPLICATION NUMBER: US/60/233,133
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,009
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,034
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,509
PRIOR FILING DATE: 2000-09-22
PRIOR APPLICATION NUMBER: US/60/234,567
PRIOR FILING DATE: 2000-09-22
NUMBER OF SEQ ID NOS: 1392
SOFTWARE: PatentIn version 3.0
SEQ ID NO 16
LENGTH: 3076
TYPE: DNA
ORGANISM: Homo sapiens

US-09-954-531-16

Query Match 27.5%; Score 56; DB 9; Length 3076;
Best Local Similarity 55.0%; Pred. No. 4.5e-08;
Matches 110; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
Qy 1 GAGTTTAATAGATTAAACATTTTGGCTAATTTTCCAACTGGTAGTCCCTGTTTCAGCATCA 60
Db 809 GAACGTGTACCGAATGCTACGTAATCCACTTTTCTGCTGGGTTCCTGCTCAGAAAGG 868
Qy 61 ACACCTGGCAGCAGGAGGTTTCTTTATCTACTGGTGNAGAGATACCGTCCGGTGGCTTTAGT 120
Db 869 AGTCTTGCTGCTGGTGTCTTATACACTGGTGTGAATGACAGGTCAAAATGCTTCTGT 928
Qy 121 TGTCTATGACGTGTAGATAGATGGAATATGAGACTCAGCAGTGTGGAAGACACAGGAAA 180
Db 929 TGTGGCTGTAGTGGATACTGGAAAGAGAGAGACAGTCTTACTGAAAGCATATAAAG 988
Qy 181 GTATCCCCAAATTCAGATT 200
Db 989 TTGTATCCTAGTCAGATT 1008

RESULT 12

US-09-954-456-1635
Sequence 1635, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: PatentIn version 3.0
SEQ ID NO 1635
LENGTH: 3076
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-1635

Query Match 27.5%; Score 56; DB 10; Length 3076;
Best Local Similarity 55.0%; Pred. No. 4.5e-08;
Matches 110; Conservative 0; Mismatches 90; Indels 0; Gaps 0;
Qy 1 GAGTTTAATAGATTAAACATTTTGGCTAATTTTCCAACTGGTAGTCCCTGTTTCAGCATCA 60
Db 809 GAACGTGTACCGAATGCTACGTAATCCACTTTTCTGCTGGGTTCCTGCTCAGAAAGG 868
Qy 61 ACACCTGGCAGCAGGAGGTTTCTTTATCTACTGGTGNAGAGATACCGTCCGGTGGCTTTAGT 120
Db 869 AGTCTTGCTGCTGGTGTCTTATACACTGGTGTGAATGACAGGTCAAAATGCTTCTGT 928

QY 121 TGTATGACGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
Db 929 TGTGGCCTGATGCTGGATGAATGGAAGAGAGAGACAGTCTACTGAAAGCATATAAAAG 988
QY 181 GTATCCCAAAATTCAGATT 200
Db 989 TTGTATCCTAGCTGCAGATT 1008

RESULT 13
US-09-974-592-f
; Sequence 5, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6669
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: variation
; LOCATION: (3677)...(3951)
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-5

Query Match 27.5%; Score 56; DB 10; Length 6669;
Best Local Similarity 55.08; Pred. No. 6.7e-08;
Matches 110; Conservative 0; Mismatches 90; Indels 0; Gaps 0:

QY 1 GAGTTTAATAGATTAATAAATTTGCTAATTTTCCAACTGGTAGTCCCTGTTTCAGCATCA 60
Db 4305 GAACGTGTACCGAATGCTACGTATATCCACTTTTCTGCTGGGTTCCCTGCTCAGAAAGG 4364
QY 61 ACACGTGGCAGCAGCAGGCTTTCTTTATCTAGTGTGAAGAGATACCGTGGGCTGCTTTAGT 120
Db 4365 AGTCTGTCTGCTGGTGGTCTTATACACTGTGTGAATGACAAGGTCAAAATGCTTCTGT 4424
QY 121 TGTATGACGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
Db 4425 TGTGGCCTGATGCTGGATAGTGGAAAGAGAGAGACAGTCTACTGAAAGCATATAAAAG 4484
QY 181 GTATCCCAAAATTCAGATT 200
Db 4485 TTGTATCCTAGCTGCAGATT 4504

RESULT 14
US-09-201-936-7
; Sequence 7, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter

; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; PRIOR FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2412)...(2412)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-7

Query Match 27.4%; Score 55.8; DB 9; Length 2580;
Best Local Similarity 54.7%; Pred. No. 4.8e-08;
Matches 111; Conservative 0; Mismatches 92; Indels 0; Gaps 0:

QY 1 GAGTTTAATAGATTAATAAATTTGCTAATTTTCCAACTGGTAGTCCCTGTTTCAGCATCA 60
Db 373 GACTCTACAGATGCTACATATTTCAACTTTCCCGCGGGTCTGCTCAGAAAGG 432
QY 61 ACACGTGGCAGCAGCAGGCTTTCTTTATCTAGTGTGAAGAGATACCGTGGGCTGCTTTAGT 120
Db 433 AGTCTGTCTGCTGGTGGTCTTATATATATATGCTGTGAATGACAAGGTCAAAATGCTTCTGT 492
QY 121 TGTATGACGCTGTAGATAGATGCAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 180
Db 493 TGTGGCCTGATGCTGGATAGTGGAACTAGAGACAGTCTCTATTCAAAGCATATAACAG 552
QY 181 GTATCCCAAAATTCAGATT 203
Db 553 CTATATCCTAGCTGTAGCTTTAT 575

RESULT 15
US-09-880-107-3354
; Sequence 3354, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3354
; LENGTH: 3532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U37547
US-09-880-107-3354

GenCore version 5.1.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:12:47 ; Search time 976.083 Seconds

(without alignments)
3384.833 Million cell updates/sec

Title: US-09-654-743-45

Perfect score: 204

Sequence: 1 gaggtttaacagattaaaac.....ccccaaattgcagattttac 204

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2:  em_esthum:*
3:  em_estlin:*
4:  em_estnu:*
5:  em_estov:*
6:  em_estpl:*
7:  em_estro:*
8:  em_htc:*
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11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
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24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	100.0	529	9	AL713196
2	204	100.0	1041	13	BM459898
3	193	94.6	852	14	BQ423165
4	170.4	83.5	698	10	BB653654
5	129	63.2	822	12	BG502660
6	111.4	54.6	575	13	BM489612

7	103	50.5	676	13	BI392530
8	93.2	45.7	603	9	AL646185
9	91.6	44.9	593	13	BJ096099
10	91.6	44.9	681	12	BF611032
11	90.6	44.4	530	13	BJ030180
12	85.2	41.8	603	12	BF614726
13	73.8	36.2	300	9	AU098645
14	69	33.8	756	12	BG773530
15	68.4	33.5	1130	13	BM553272
16	66.8	32.7	742	13	BI829221
17	66.8	32.7	1020	13	BM554544
18	66.4	32.5	557	13	BI475879
19	66.4	32.5	562	13	BI706974
20	66.4	32.5	565	13	BI706975
21	66.4	32.5	676	12	BF156225
22	64.8	31.8	574	13	BI706911
23	64.4	31.6	624	14	BQ552033
24	64.2	31.5	746	9	AF160669
25	63.6	31.2	535	14	BQ618784
26	63.6	31.2	594	12	BF158160
27	63.6	31.2	658	13	BM157229
28	62.2	30.5	569	12	BG082235
29	62.2	30.5	633	12	BE912864
30	62.2	30.5	669	10	BB625247
31	62.2	30.5	884	13	BI104522
32	60.4	29.6	828	13	BI463479
33	59.2	29.0	475	12	BF615511
34	58.8	28.0	767	13	BI876215
35	58.4	28.6	196	13	BI875741
36	57.8	28.3	801	13	BG934097
37	57.2	28.0	550	12	BF021480
38	57	27.9	613	14	BQ391082
39	57	27.9	644	14	BQ389388
40	56	27.5	590	10	AW500255
41	56	27.5	959	13	BM458775
42	55.8	27.4	464	14	BM753271
43	55.8	27.4	837	12	BG743309
44	55.8	27.4	855	9	AU131149
45	55.8	27.4	891	12	BE886741

ALIGNMENTS

RESULT 1	AL713196	529 bp	mrna	linear	EST 22-MAR-2002
LOCUS	DKFZp686M1895_r1	686	(synonym: hicc3)	Homo sapiens	cdna clone
DEFINITION	DKFZp686M1895 5', mRNA sequence.				
ACCESSION	AL713196				
VERSION	AL713196.1	GI:19696552			
KEYWORDS	EST.				
SOURCE	human.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
	1 (bases 1 to 529)				
	Bloecher,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and Wiemann				
TITLE	EST (Bloecher,H., Boecher,M., Brandt,P., Mewes,H.W., Weil,B. and				
JOURNAL	Wiemann,S.)				
COMMENT	Unpublished (1999)				
	Contact: Bloecker H				
	MFPS				
	Am Klopferstritz 18a D-82152 Martinsried, Germany				
	This is the 5' sequence of the clone insert				
	Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer				
	Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;				
	Sequenced by GBF (National Research Centre for Biotechnology Ltd.,				
	Braunschweig/Germany) within the cdna sequencing consortium of the				
	German Genome Project.				
	No sl sequence available.				
	This clone (DKFZp686M1895) is available at the RZPD in Berlin.				

Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES

source

1. 529
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="DKF2686M1895"
/clone_lib="686 (synonym: hlcc3)"
/tissue_type="human skeletal muscle"
/dev_stage="adult"
/lab_host="DH10B"
/note="vector: pTriplEx2; Site_1: SfiII; Site_2: SfiIB;
cdna collection"

BASE COUNT 165 a 96 c 126 g 142 t

ORIGIN

Query Match 100.0%; Score 204; DB 9; Length 529;
Best Local Similarity 100.0%; Pred. No. 8.1e-54; Indels 0; Gaps 0;
Matches 204; Conservative 0; Mismatches 0;

Qy 1 GAGTTTAATAGATTAAACATTTTCTTAATTTCCAGTGGTAGTCCTGTTTCAGCATCA 60

Db 137 GAGTTTAATAGATTAAACATTTTCTTAATTTCCAGTGGTAGTCCTGTTTCAGCATCA 196

Qy 61 ACATGGCAGCAGCAGGGTCTTTTATCTGTTGAGAGATACCGTGGTGGCTTTTACT 120

Db 197 ACATGGCAGCAGCAGGGTCTTTTATCTGTTGAGAGATACCGTGGTGGCTTTTACT 256

Qy 121 TGTCTATGAGCTGTAGATAGATGCAATATGAGACTCAGCAGTTGGAGACACAGGAAA 180

Db 257 TGTCTATGAGCTGTAGATAGATGCAATATGAGACTCAGCAGTTGGAGACACAGGAAA 316

Qy 181 GTATCCCCAAATTCGAGATTATC 204

Db 317 GTATCCCCAAATTCGAGATTATC 340

RESULT 2

BM459898

LOCUS BM459898 1041 bp mRNA linear EST 05-FEB-2002

DEFINITION AGNCOURT_6422054 NIH_MGC_71 Homo sapiens cdna clone IMAGE:5532247

5', mRNA sequence.

ACCESSION BM459898

VERSION BM459898.1 GI:18508938

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1041)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@rs-re@mail.nih.gov

Tissue Procurement: ATCC

cdna Library Preparation: Life Technologies, Inc.

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM12215 row: d column: 08

High quality sequence stop: 567.

Location/Qualifiers

1..1041

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5532247"

/clone_lib="NIH_MGC_71"

/tissue_type="leiomyosarcoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2.1 kb.

BASE COUNT 297 a 208 c 266 g 269 t

ORIGIN

Query Match 100.0%; Score 204; DB 13; Length 1041;

Best Local Similarity 100.0%; Pred. No. 1.1e-53;

Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 GAGTTTAATAGATTAAACATTTTCTTAATTTCCAGTGGTAGTCCTGTTTCAGCATCA 60

Db 142 GAGTTTAATAGATTAAACATTTTCTTAATTTCCAGTGGTAGTCCTGTTTCAGCATCA 201

Qy 61 ACATGGCAGCAGCAGGGTCTTTTATCTGTTGAGAGATACCGTGGTGGCTTTTACT 120

Db 202 ACATGGCAGCAGCAGGGTCTTTTATCTGTTGAGAGATACCGTGGTGGCTTTTACT 261

Qy 121 TGTCTATGAGCTGTAGATAGATGCAATATGAGACTCAGCAGTTGGAGACACAGGAAA 180

Db 262 TGTCTATGAGCTGTAGATAGATGCAATATGAGACTCAGCAGTTGGAGACACAGGAAA 321

Qy 181 GTATCCCCAAATTCGAGATTATC 204

Db 322 GTATCCCCAAATTCGAGATTATC 345

RESULT 3

BQ423165

LOCUS BQ423165

DEFINITION AGNCOURT_7761069 NIH_MGC_72 Homo sapiens

5', mRNA sequence.

ACCESSION BQ423165

VERSION BQ423165.1 GI:21118480

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 852)

NIH-MGC http://mgs.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cga@rs-re@mail.nih.gov

Tissue Procurement: ATCC/DCFD/PTP

cdna Library Preparation: Life Technologies, Inc.

cdna Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone Distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM13332 row: m column: 14

High quality sequence stop: 503.

Location/Qualifiers

1..852

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:6062005"

/clone_lib="NIH_MGC_72"

/tissue_type="melanotic melanoma"

/lab_host="DH10B (phage-resistant)"

/note="Organ: skin; Vector: pCMV-SPORT6; Site_1: NotI;

Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 2 kb. Library constructed by Life

Technologies."

Location/Qualifiers

210 a 191 c 242 g 209 t

BASE COUNT

ORIGIN

Query Match 94.6%; Score 193; DB 14; Length 852;

Best Local Similarity 99.5%; Pred. No. 3.1e-50;

Matches 204; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 GAGTTTAATAGATTAAACATTTTCTTAATTTCCAGTGGTAGTCCTGTTTCAGCATCA 60

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone Distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLCMI449 row: c column: 23
 High quality sequence stop: 670.
 Location/Qualifiers

FEATURES

source

1. .822
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4657102"
 /clone_lib="NIH_MGC_61"
 /tissue_type="embryonal carcinoma"
 /lab_host="DH10B (TI phage-resistant)"
 /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
 SfiI (ggcgctcgcc); Site_2: SfiI (ggcattatggcc);
 Double-stranded cDNA was prepared from cell line RNA. 5'
 and 3' adaptors were used in cloning as follows: 5'
 adaptor sequence: 5'-ATTCTAGAGCGGCGCCGACATG-dT(30)BN-3'
 (where B = A, C, or G and N = A, C, G, or T). Average
 insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
 contained inserts by PCR. This library was enriched for
 full-length clones and was constructed by Clontech
 Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
 Library."

BASE COUNT 236 a 161 c 201 g 222 t 2 others
 ORIGIN
 Query Match 63.2%; Score 129; DB 12; Length 822;
 Best Local Similarity 100.0%; Pred. No. 5.9e-30;
 Matches 129; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 76 GGGTTCTTTTACTGTTGAAGGAGATACCGTGGCGTCTTAGTTGTTCATGCACCTGTA 135
 Db 1 GGGTTCTTTTACTGTTGAAGGAGATACCGTGGCGTCTTAGTTGTTCATGCACCTGTA 60
 Qy 136 GATAGATGGCAATATGGAGACTACAGTTGGAGACACAGAAAGTATCCCAATATGC 195
 Db 61 GATAGATGGCAATATGGAGACTACAGTTGGAGACACAGAAAGTATCCCAATATGC 120
 Qy 196 AGATTATC 204
 Db 121 AGATTATC 129

RESULT 6
 BM489612 575 bp mRNA linear EST 07-FEB-2002
 LOCUS
 DEFINITION pgm2n.pk011.h2 Normalized Chicken Breast Muscle, Leg Muscle, and
 Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA
 clone pgm2n.pk011.h2 5', similar to gb|AA47170.1|AF451854.1
 (AF451854) inhibitor of apoptosis protein 3 [Gallus gallus], mRNA
 sequence.

ACCESSION BM489612
 VERSION BM489612.1 GI:18610543
 KEYWORDS EST.
 SOURCE chicken.
 ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 575)
 AUTHORS Cogburn, L.A. and Monsonego-Ornan, E.
 TITLE ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and
 Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
 Project

JOURNAL Unpublished (2002)
 COMMENT Contact: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335

Fax: 302-831-2822
 Email: cogburn@udel.edu, www.chickest.udel.edu.
 Location/Qualifiers

FEATURES

source

1. .575
 /organism="Gallus gallus"
 /strain="Commercial broiler and Ottawa Res. Centre
 Strains 90 & 21"
 /db_xref="taxon:9031"
 /clone="pgm2n.pk011.h2"
 /clone_lib="Normalized Chicken Breast Muscle, Leg Muscle,
 and Epiphyseal Growth Plate cDNA library (pgm2n)"
 /sex="Male and Female"
 /tissue_type="Breast muscle, leg muscle and epiphyseal
 growth plate"
 /dev_stage="Breast, leg; Embryo(d19); post-hatch(1d,1.3,5,7,9
 ,11 weeks); growth plate(1d,7d,14d post-hatch)"
 /lab_host="E. coli EMDH10B"
 /note="Vector: pCMVSPORT6; Library made from equivalent
 pools of total RNA isolated from each tissue (embryonic
 muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth
 plate 33.3% of the final RNA pool). Single pass sequencing
 from 5'-end"

BASE COUNT 144 a 131 c 152 g 145 t 3 others
 ORIGIN

Query Match 54.6%; Score 111.4; DB 13; Length 575;
 Best Local Similarity 73.6%; Pred. No. 1.9e-24;
 Matches 142; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

Qy 11 GATTAATAAACTTTTGTCTTAATTTTCCAAAGTGTAGTCCTTTTCAGCATCAACACTGGCAC 70
 Db 138 GACTAGGAACCTTTTGTGAGTTTCCCATGATGTCCTTCAGCATCAGCGTAGCTC 197
 Qy 71 GAGCAGGGTTCTTTATCTACTGTTGAAGGAGATACCGTGGCGTCTTAGTTGTCTGTCAG 130
 Db 198 GAGCTGGCTTTTATCTACTGTTGAAGGAGTATAAAGTCAAGTGCCTTCAGTGCATGTAA 257
 Qy 131 CTGTAGATAGATGGCAATATGGAGACTACAGTGGAGACACAGAAAGTATCCCCAA 190
 Db 258 CTGTTGAAGGATGGAGCCTGGGGATTCTGCAATTGACAGACACAAAACCTTTCCCCCAG 317
 Qy 191 ATTGCAGATTTAT 203
 Db 318 ATTGCAGATTTAT 330

RESULT 7
 BI392530 676 bp mRNA linear EST 06-AUG-2001
 LOCUS
 DEFINITION pgpin.pk008.d6 Normalized Chicken Pituitary/Hypothalamus/Pineal
 Library Gallus gallus cDNA clone pgpin.pk008.d6 5', similar to
 gb|AAG22969.1|AF183429.1 (AF183429) inhibitor of apoptosis protein
 3 [Rattus norvegicus], mRNA sequence.

ACCESSION BI392530
 VERSION BI392530.1 GI:15085812
 KEYWORDS EST.
 SOURCE chicken.
 ORGANISM Gallus gallus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
 Phasianinae; Gallus.

REFERENCE 1 (bases 1 to 676)
 AUTHORS Porter, T.E. and Cogburn, L.A.
 TITLE ESTs from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
 library USDA/IFAFS Animal Genome Project

JOURNAL Unpublished (2001)
 COMMENT Contact: Larry A. Cogburn
 University of Delaware
 Townsend Hall, Newark, DE 19717, USA
 Tel: 302-831-1335
 Fax: 302-831-2822
 Email: cogburn@udel.edu, www.chickest.udel.edu.
 Location/Qualifiers

Query Match 44.9%; Score 91.6; DB 12; Length 681;
Best Local Similarity 67.0%; Pred. No. 3.9e-18;

LOCUS BG773530 756 bp mRNA linear EST 15-MAY-2001
 DEFINITION 602720264F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4837478 5',
 mRNA sequence.
 ACCESSION BG773530
 VERSION BG773530.1 GI:14084183
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 756)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaops-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 Toshiyuki and Piero Carninci (RIKEN)
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM10769 row: o column: 15
 High quality sequence stop: 740.
 FEATURES
 source
 1..756
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:4837478"
 /clone_lib="NIH_MGC_97"
 /lab_host="DH10B"
 /note="Organ: testis; Vector: pBluescriptR (modified
 pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTVN-3',
 size-selected for average insert size 2.2 kb and
 normalized to ROT 5. This is a primary library enriched
 for full-length clones and constructed using the
 Cap-trapper method (Carninci, in preparation). Library
 constructed by M. Brownstein (NIH/NHGRI, National
 Institutes of Health). Note: this is a NIH_MGC Library."
 BASE COUNT 166 a 181 c 245 g 163 t 1 others
 ORIGIN
 Query Match 33.8%; Score 69; DB 12; Length 756;
 Best Local Similarity 64.7%; Pred. No. 6e-11;
 Matches 132; Conservative 0; Mismatches 46; Indels 26; Gaps 1;
 QY 1 GAGTTTAATAGATTAAAACTTTTCTTAATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 60
 DB 384 GAGATTATAGATCAAAACAGTTTCTGCTTTGAGTGGTGGCCCTCGCTGGGCATCG 443
 QY 61 ACACGTGGCAGCAGGAGGTTTCTTTATACGTGGTGAAGAGATACCGTCGGTGTCTTAGT 120
 DB 444 GCGC-----GNTGAGGAGAGCGCCCTGGGGGCGCTTAGC 477
 QY 121 TGTCTATGACGTCTAGATAGATGGCAATATGGAGACTCAGCGTTGGAGACACAGGAAA 180
 DB 478 TGCCCTGAAGCGGTAGACAGGTGGCAAGCTGGGGGCTCAGGAGTTGACAAACACAGAAA 537
 QY 181 GTATCCCAAAATTCGAGATTATTC 204
 DB 538 GCAGCGCCGAATTCGAGGTTTATC 561
 RESULT 15
 BM553272
 LOCUS BM553272 1130 bp mRNA linear EST 20-FEB-2002
 DEFINITION AGENCOURT_6542515 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742924
 5', mRNA sequence.
 ACCESSION BM553272
 VERSION BM553272.1 GI:18791860

KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1130)
 NIH-MGC http://mgi.nci.nih.gov/
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgaops-r@mail.nih.gov
 Tissue Procurement: Life Technologies, Inc.
 cDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLAM12761 row: n column: 13
 High quality sequence stop: 691.
 FEATURES
 source
 1..1130
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="IMAGE:5742924"
 /clone_lib="NIH_MGC_119"
 /tissue_type="medulla"
 /lab_host="DH10B"
 /note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
 Site_2: EcoRV (destroyed); RNA source normal medulla from
 anonymous male age 27. Library is oligo-dT primed and
 directionally cloned (EcoRV site is destroyed upon
 cloning). Average insert size 1.3 kb, insert size range
 0.9-3 kb. Library is normalized and enriched for
 full-length clones and was constructed by C. Gruber
 (Invitrogen). Research Genetics tracking code 013. Note:
 this is a NIH_MGC Library."
 BASE COUNT 257 a 267 c 343 g 261 t 2 others
 ORIGIN
 Query Match 33.5%; Score 68.4; DB 13; Length 1130;
 Best Local Similarity 64.7%; Pred. No. 1.1e-10;
 Matches 132; Conservative 0; Mismatches 46; Indels 26; Gaps 1;
 QY 1 GAGTTTAATAGATTAAAACTTTTCTTAATTTTCCAAAGTGGTAGTCCTGTTTCAGCATCA 60
 DB 391 GAGATTATAGATCAAAACAGTTTCTGCTTTGAGTGGTGGCCCTCGCTGGGCATCG 450
 QY 61 ACACGTGGCAGCAGGAGGTTTCTTTATACGTGGTGAAGAGATACCGTCGGTGTCTTAGT 120
 DB 451 GCGC-----GTTGAGGAGAGCGCCCTGGGGGCGCTTAGC 484
 QY 121 TGTCTATGACGTCTAGATAGATGGCAATATGGAGACTCAGCAGTTGGAGACACAGGAAA 180
 DB 485 TGCCCTGAAGCGGTAGACAGGTGGCAAGCTGGGGGCTCAGGAGTTGACAAACACAGAAA 544
 QY 181 GTATCCCAAAATTCGAGATTATTC 204
 DB 545 GCAGCGCCGAATTCGAGGTTTATC 568
 Search completed: April 16, 2003, 00:54:50
 Job time : 983.083 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:40:42 ; Search time 1031.86 seconds
(without alignments)
5753.635 Million cell updates/sec

Title: US-09-654-743-46
Perfect score: 204
Sequence: 1 gaagaagctagattaaagtc.....ttcttaattgctctttgtt 204

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1:	gb_ba.*	GenBank
2:	gb_hgt.*	GenBank
3:	gb_in.*	GenBank
4:	gb_om.*	GenBank
5:	gb_ov.*	GenBank
6:	gb_pat.*	GenBank
7:	gb_ph.*	GenBank
8:	gb_pl.*	GenBank
9:	gb_pr.*	GenBank
10:	gb_ro.*	GenBank
11:	gb_sts.*	GenBank
12:	gb_sy.*	GenBank
13:	gb_un.*	GenBank
14:	gb_vl.*	GenBank
15:	em_ba.*	EMBL
16:	em_fun.*	EMBL
17:	em_hum.*	EMBL
18:	em_in.*	EMBL
19:	em_mu.*	EMBL
20:	em_om.*	EMBL
21:	em_or.*	EMBL
22:	em_ov.*	EMBL
23:	em_pat.*	EMBL
24:	em_ph.*	EMBL
25:	em_pl.*	EMBL
26:	em_ro.*	EMBL
27:	em_sts.*	EMBL
28:	em_un.*	EMBL
29:	em_vl.*	EMBL
30:	em_htg_hum.*	EMBL
31:	em_htg_inv.*	EMBL
32:	em_htg_other.*	EMBL
33:	em_htg_mus.*	EMBL
34:	em_htg_pln.*	EMBL
35:	em_htg_rnd.*	EMBL
36:	em_htg_mam.*	EMBL
37:	em_htg_vrt.*	EMBL
38:	em_sy.*	EMBL
39:	em_htgo_hum.*	EMBL
40:	em_htgo_mus.*	EMBL
41:	em_htgo_other.*	EMBL

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	204	100.0	1659	6	E31042	E31042 Method for
2	204	100.0	1659	9	HSU32974	U32974 Human IAP-1
3	204	100.0	2086	9	BC032729	BC032729 Homo sapi
4	204	100.0	2540	6	AR103281	AR103281 Sequence
5	204	100.0	2540	6	AX412118	AX412118 Sequence
6	204	100.0	2540	9	HSU45880	U45880 Human X-lin
7	204	100.0	3000	6	AX412131	AX412131 Sequence
8	204	100.0	5232	6	AR106397	AR106397 Sequence
9	204	100.0	5232	6	AR116699	AR116699 Sequence
10	204	100.0	133391	9	HSU315G1	U121601 Human DNA
11	204	100.0	201197	2	HS424J12	282207 Homo sapien
12	193	94.6	2404	6	AX429575	AX429575 Sequence
13	172	84.3	2100	6	AX412124	AX412124 Sequence
14	172	84.3	2691	6	AR106400	AR106400 Sequence
15	172	84.3	2691	6	AR116702	AR116702 Sequence
16	172	84.3	2691	10	MMU88990	U88990 Mus musculu
17	170.4	83.5	1988	10	MMU36842	U36842 Mus musculu
18	167.2	82.0	2032	10	AF304333	AF304333 Rattus no
19	167.2	82.0	2468	10	AB033366	AB033366 Rattus no
20	167.2	82.0	3032	10	AF304334	AF304334 Rattus no
21	165.6	81.2	1491	10	AF183429	AF183429 Rattus no
22	165.6	81.2	1758	6	AX370787	AX370787 Sequence
23	164	80.4	1758	6	AX370789	AX370789 Sequence
24	164	80.4	2032	9	AF420440	AF420440 Homo sapi
25	164	80.4	4993	6	AX104968	AX104968 Sequence
26	164	80.4	4993	9	AF164682	AF164682 Homo sapi
27	164	80.4	144301	9	AC010467	AC010467 Homo sapi
28	164	80.4	165662	9	AC092070	AC092070 Homo sapi
29	141	69.1	184439	2	AP003085	AP003085 Homo sapi
30	141	69.1	187568	9	AP002967	AP002967 Homo sapi
31	138.4	67.8	7990	6	AX281265	AX281265 Sequence
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36	84.6	41.5	2563	9	HUMSCP8	L49432 Homo sapien
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38	84.6	41.5	2676	6	AX412120	AX412120 Sequence
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41	84.6	41.5	3076	6	AX330574	AX330574 Sequence
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43	84.6	41.5	3076	9	HSU37546	U37546 Human IAP h
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45	84.6	41.5	3734	6	AX472621	AX472621 Sequence

ALIGNMENTS

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E31042	E31042	1659 bp	DNA	linear	PAT 18-JUN-2001
LOCUS	E31042	Method for screening substance inhibiting binding to XIAP.			
DEFINITION	E31042				
ACCESSION	E31042				
VERSION	E31042.1	GI:13017307			
KEYWORDS	JP 1999326328-A/2.				
SOURCE	unidentified.				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 1659)				
AUTHORS	Kunihiro,M.				
TITLE	Method for screening substance inhibiting binding to XIAP				
JOURNAL	Patent: JP 1999326328-A 2 26-NOV-1999;				
	KUNIHIRO MATSUMOTO				

```

COMMENT OS Unidentified
PN JP 199328328-A/2
PD 26-NOV-1999
PF 13-NOV-1998 JP 1998130378
PR KUNIHIO MATSUMOTO
PC G01N33/536, A61K38/00, A61K38/00, A61K38/00, A61K38/00, A61K38/22,
PC A61K39/395, A61K38/00, A61K38/00, A61K45/00, C07K7/06, C07K7/08, C07K14/47, PC
PC A61K45/00, A61K45/00, A61K45/00, A61K45/00, C12N15/09, C12P21/08, A61K37/02,
G01N33/536,
PC G01N33/536, G01N33/536//C12N15/09, C12P21/08, A61K37/02,
A61K37/02, PC A61K37/02,
PC A61K37/02, A61K37/24, C12N15/00
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CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 82..1572.
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source Location/Qualifiers
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BASE COUNT 519 a 296 c 385 g 459 t
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Best Local Similarity 100.0%; Pred. No. 3.4e-56;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAGAAGCTAGATTAAAGTCTCTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60
DB 568 GAAGAAGCTAGATTAAAGTCTCTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 627
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DB 628 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATGTTGACCAAGTGCAGTGTCTTTGT 687
QY 121 TGTGTGAAACCTGAAATTTGGAACTTGTGATCGTCTGCTGACAGACACAGGCGA 180
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RESULT 2
HSU32974 1659 bp mRNA linear PRI 12-JUN-1996
LOCUS Human IAP-like protein ILP mRNA, complete cds.
DEFINITION
ACCESSION U32974
VERSION U32974.1 GI:1016687
KEYWORDS apoptosis; ring finger; zinc finger.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 1659)
Duckett,C.S., Nava,V.E., Gedrich,R.W., Clem,R.J., Van Dongen,J.L.,
Gilfillan,M.C., Shiels,H., Hardwick,J.M. and Thompson,C.B.
A conserved family of cellular genes related to the baculovirus iap
gene and encoding apoptosis inhibitors
EMBO J. 15 (11), 2685-2694 (1996)
JOURNAL
MEDLINE 96256286
PUBMED 8654366
REFERENCE
2 (bases 1 to 1659)
Duckett,C.S. and Thompson,C.B.
Direct Submission
AUTHORS
TITLE
Submitted (01-AUG-1995) Colin Duckett, Howard Hughes Medical
Institute, The University of Chicago, 924 East 57th Street,
Chicago, IL 60637, USA
JOURNAL
LOCATION/Qualifiers
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misc_feature 877..1068
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misc_feature 1420..1542
/note="RING finger"
BASE COUNT 519 a 296 c 385 g 459 t
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Best Local Similarity 100.0%; Pred. No. 3.4e-56;
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QY 1 GAAGAAGCTAGATTAAAGTCTCTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60
DB 568 GAAGAAGCTAGATTAAAGTCTCTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 627
QY 61 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATGTTGACCAAGTGCAGTGTCTTTGT 120
DB 628 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATGTTGACCAAGTGCAGTGTCTTTGT 687
QY 121 TGTGTGAAACCTGAAATTTGGAACTTGTGATCGTCTGCTGACAGACACAGGCGA 180
DB 688 TGTGTGAAACCTGAAATTTGGAACTTGTGATCGTCTGCTGACAGACACAGGCGA 747
QY 181 CACTTTCCTAATGCTCTCTTTGTT 204
DB 748 CACTTTCCTAATGCTCTCTTTGTT 771
RESULT 3
BC032729 2086 bp mRNA linear PRI 27-JUN-2002
LOCUS IMAGE:5532247, mRNA, complete cds.
DEFINITION
ACCESSION BC032729
VERSION BC032729.1 GI:21619763
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 2086)
Strausberg,R.
Direct Submission
AUTHORS
TITLE
Submitted (06-JUN-2002) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
REMARK
NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT
Contact: MGC help desk
Email: cgapbs-remail.nih.gov

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Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc_mgc@hgrl.nih.gov/
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Masiello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
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 This clone was selected for full length sequencing because it
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 QY 121 TGTGTGGAAACTGAAATAATGGGAACTTGTGATCGCTGCTGCTGACCAAGCAGGCGCA 180
 Db 685 TGTGTGGAAACTGAAATAATGGGAACTTGTGATCGCTGCTGCTGACCAAGCAGGCGCA 744
 QY 181 CACTTTCCTTAATGCTCTCTTTGTT 204
 Db 745 CACTTTCCTTAATGCTCTCTTTGTT 768
 RESULT 4
 AR103281
 LOCUS 2540 bp DNA linear PAT 14-FEB-2001

DEFINITION Sequence 1 from patent US 6087173.
 ACCESSION AR103281
 VERSION AR103281.1 GI:12814869
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 2540)
 AUTHORS Bennett, C. Frank., Ackermann, E.J. and Cowser, L.M.
 TITLE Antisense modulation of X-linked inhibitor of apoptosis expression
 JOURNAL Patent: US 6087173-A 1 11-JUL-2000;
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 Db 580 GAGTTAGCAAGTCGTGGACTCTACTACAGAGTATTGGTGACCAAGTCAGTGCCTTTTGT 639
 QY 121 TGTGTGGAAACTGAAATAATGGGAACTTGTGATCGCTGCTGCTGACCAAGCAGGCGCA 180
 Db 640 TGTGTGGAAACTGAAATAATGGGAACTTGTGATCGCTGCTGCTGACCAAGCAGGCGCA 699
 QY 181 CACTTTCCTTAATGCTCTCTTTGTT 204
 Db 700 CACTTTCCTTAATGCTCTCTTTGTT 723
 RESULT 5
 AX412118 2540 bp DNA linear PAT 14-JUN-2002
 LOCUS Sequence 218 from Patent WO0226968.
 DEFINITION AX412118
 ACCESSION AX412118
 VERSION AX412118.1 GI:21444581
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1
 AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.
 TITLE Antisense iap nucleic acids and uses thereof
 JOURNAL Patent: WO 0226968-A 218 04-APR-2002;
 University of Ottawa (CA); Aegera Therapeutics Inc. (CA)
 FEATURES Location/Qualifiers
 source 1. 2540
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 Db 700 CACTTTCCTAATGCTCTTTTGGT 723

RESULT 6
 HSU45880 2540 bp mRNA linear PRI 16-FEB-1996
 LOCUS Human x-linked inhibitor of apoptosis protein XIAP mRNA, complete
 DEFINITION cds.
 VERSION 045880
 KEYWORDS
 SOURCE Homo sapiens.
 ORGANISM Homo sapiens.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 2540)
 LISTON, P., ROY, N., TAMAI, K., LEFEBVRE, C., BAIRD, S.,
 CHERTON-HORVAT, G., FARAHANI, R., McLEAN, M., IKEDA, J., MACKENZIE, A.
 and KORNELUK, R. G.
 TITLE Suppression of apoptosis in mammalian cells by NAIP and a related
 family of IAP genes
 JOURNAL Nature 379 (6563), 349-353 (1996)
 MEDLINE 96149249
 PUBMED 8552191
 REFERENCE 2 (bases 1 to 2540)
 BAIRD, S.D.
 AUTHORS Direct Submission
 TITLE Submitted (16-JAN-1996) Stephen D. Baird, Children's Hospital of
 Eastern Ontario, Genetics, 401 Smyth Rd., Ottawa, Ontario, K1H 8L1,
 Canada
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 520. 723
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 ORIGIN

Query Match 100.0%; Score 204; DB 9; Length 2540;

Best Local Similarity 100.0%; Pred. No. 3.4e-56;
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QY 1 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60
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 Db 700 CACTTTCCTAATGCTCTTTTGGT 723

RESULT 7
 AX412131 3000 bp DNA linear PAT 14-JUN-2002
 LOCUS Sequence 231 from Patent WO0226968.
 DEFINITION AX412131
 ACCESSION AX412131
 VERSION AX412131.1 GI:21444588
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1
 KORNELUK, R. G., LACASSE, E., BAIRD, S., HOLCIK, M. and YOUNG, S.
 ANTISENSE IAP NUCLEIC ACIDS AND USES THEREOF
 TITLE Patent: WO 0226968-A 231 04-APR-2002;
 JOURNAL University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
 FEATURES
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 BASE COUNT 974 a 452 c 601 g 973 t
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Query Match 100.0%; Score 204; DB 6; Length 3000;
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 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 QY 181 CACTTTCCTAATGCTCTTTTGGT 204
 Db 1356 CACTTTCCTAATGCTCTTTTGGT 1379

RESULT 8
 AR106397 5232 bp DNA linear PAT 14-FEB-2001
 LOCUS AR106397
 DEFINITION Sequence 3 from patent US 6107041.
 ACCESSION AR106397
 VERSION AR106397.1 GI:12820927
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unknown.


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Unclassified.
1 (bases 1 to 5232)
Korneluk,R.G., MacKenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and
Pratt,C.
Detection and modulation of IAPs for the diagnosis and treatment of
proliferative disease
Patent: US 6107041-A 3 22-AUG-2000;
FEATURES
Source
Location/Qualifiers
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/organism="unknown"
BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others
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Db 520 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579
QY 61 GAGTTAGCAAGTCTGGACTCTACTACACAGGATTGGTGACCAAGTGCAGTGTCTTTTGT 120
Db 580 GAGTTAGCAAGTCTGGACTCTACTACACAGGATTGGTGACCAAGTGCAGTGTCTTTTGT 639
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Db 700 CACTTTCCTAATTCCTCTTTTGT 723
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ARL16699
LOCUS ARL16699 5232 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6133437.
ACCESSION ARL16699
VERSION ARL16699.1 GI:14097021
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 5232)
AUTHORS Korneluk,R.G., MacKenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and
Pratt,C.
TITLE Modulation of IAPs for the treatment of proliferative diseases
JOURNAL Patent: US 6133437-A 3 17-OCT-2000;
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Location/Qualifiers
1..5232
/organism="unknown"
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Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 700 CACTTTCCTAATTCCTCTTTTGT 723
Unclassified.
1 (bases 1 to 5232)
Korneluk,R.G., MacKenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and
Pratt,C.
Detection and modulation of IAPs for the diagnosis and treatment of
proliferative disease
Patent: US 6107041-A 3 22-AUG-2000;
FEATURES
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Location/Qualifiers
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BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others
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Best Local Similarity 100.0%; Pred. No. 3.4e-56;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 TGTGGTGGAAACTGAAATTTGGAACTTGTGATCGTGCCTGGTGCGAAGACACAGCGCA 180
Db 640 TGTGGTGGAAACTGAAATTTGGAACTTGTGATCGTGCCTGGTGCGAAGACACAGCGCA 699
QY 181 CACTTTCCTAATTCCTCTTTTGT 204
Db 700 CACTTTCCTAATTCCTCTTTTGT 723
Db 700 CACTTTCCTAATTCCTCTTTTGT 723
RESULT 10
HSDJ315G1
LOCUS HSDJ315G1 133391 bp DNA linear PRI 23-JUN-2000
DEFINITION Human DNA sequence from clone RP1-315G1 on chromosome Xq24-25.
Contains a PDZ (DHR, GLGF) domain protein pseudogene, the API3 gene
for apoptosis inhibitor 3 (XIAP, HILP), a putative novel gene,
ESTs, STSSs, GSSs and a putative cpg island, complete sequence.
ACCESSION AL121601
VERSION AL121601.13 GI:7159760
KEYWORDS HTG; API3; CpG island; DHR; GLGF; HILP; PDZ; XIAP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 133391)
AUTHORS Grafham,D.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
COMMENT On Mar 6, 2000 this sequence version replaced gi:6983378.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/Projects/C.elegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX
RP1-315G1 is from the library RPI-1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
This sequence is the entire insert of clone RP1-315G1 The true
right end of clone RP6-30A23 is at 100 in this sequence.
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Best Local Similarity 100.0%; Pred. No. 3.2e-56;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GAGTTAGCAAGTGGTGGACTCTACTACACAGGTATTGGTGCCAGTGCAGTGTGTTTGT 120
|||||
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QY 121 TGTGGTGGAAAACTGAAAAATTGGGAACCTTGTGATCGTGGCTGATCAGAACACAGGCGA 180

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BASE COUNT	417 C	482 G	580 C
ORIGIN			

BASE COUNT	417 C	482 G	580 C
ORIGIN			

ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Korneluk,R.G., MacKenzie,A.E., Liston,P., Baird,S., Tsang,B.K. and Pratt,C.
TITLE Modulation of IAPs for the treatment of proliferative diseases
JOURNAL Patent: US 6133437-A 9 17-OCT-2000;
FEATURES Location/Qualifiers
1..2691
Source /organism="unknown"
BASE COUNT 819 a 479 c 562 g 831 t
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Best Local Similarity 90.2%; Pred. No. 1.2e-45;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
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Db 1158 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCCGAGACTATGCTCAATTAAACCCCAAGA 1217
Qy 61 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTTGT 120
Db 1218 GAGTTAGTCTAGTGTGGCTCTACTACACAGGGCTGATGATCAAGTGCATGCTTTTGT 1277
Qy 121 TGTGTGGAAACCTGAAAAATTGGGAACCTTGTGATCGTGTGCTGAGAACACACAGGCGA 180
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Qy 181 CACTTTCCTAATTGCTTCTTTGTT 204
Db 1338 CACTTTCCTAATTGCTTCTTTGTT 1361

Search completed: April 15, 2003, 23:23:52
Job time : 1068.86 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:38:17 ; Search time 136.354 Seconds

(without alignments)

3369.223 Million cell updates/sec

Title: US-09-654-743-46

Perfect score: 204

Sequence: 1 gaagaactagattaaagtc.....ttcctaattgtttttgtt 204

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_101002.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	100.0	1659	21	AAZ48862 Human XIAP coding
2	204	100.0	2540	18	AAZ70836 Human apoptosis in
3	204	100.0	2540	21	AAA64901 Human X-linked inh
4	204	100.0	2540	24	ABK93869 Human CDNA encodin
5	204	100.0	3000	24	ABK93875 Human CDNA encodin
6	204	100.0	5232	19	AAV55038 Human XIAP coding
7	193	94.6	2404	24	AAK99405 DNA of APP related
8	172	84.3	2100	18	AAZ70839 Mouse apoptosis in
9	172	84.3	2100	24	ABK93872 Mouse CDNA encodin

10	172	84.3	2691	19	AAV55041
11	170.4	83.5	1988	18	AAZ72710
12	165.6	81.2	1758	24	ABK14677
13	164	80.4	1559	24	ABK13197
14	164	80.4	1758	24	ABK14678
15	164	80.4	4993	22	AAZ03581
16	138.4	67.8	7990	24	ABL54307
17	138.4	67.8	7990	24	ABL32158
18	129.4	63.4	7990	24	ABL54308
19	129.4	63.4	7990	24	ABL32159
20	84.6	41.5	2601	18	AAZ61591
21	84.6	41.5	2666	18	AAZ70837
22	84.6	41.5	2676	24	ABK93870
23	84.6	41.5	3076	24	AAZ72712
24	84.6	41.5	3076	20	AAZ41005
25	84.6	41.5	3076	20	AAZ22096
26	84.6	41.5	3076	24	ABL62746
27	84.6	41.5	3076	24	ABL66325
28	84.6	41.5	3734	22	AAZ09972
29	84.6	41.5	3734	24	ABK53387
30	84.6	41.5	6669	19	AAV55039
31	84.6	41.5	6669	24	ABK93876
32	74.4	36.5	2862	18	AAZ61592
33	74.4	36.5	3151	19	AAV55043
34	72.8	35.7	2416	18	AAZ70841
35	72.8	35.7	2416	24	ABK93874
36	70.2	34.4	2291	22	AAZ08025
37	70.2	34.4	2580	18	AAZ70838
38	70.2	34.4	2580	24	ABK93871
39	70.2	34.4	2589	18	AAZ61590
40	70.2	34.4	3532	18	AAZ72711
41	70.2	34.4	3532	20	AAZ22143
42	70.2	34.4	3532	24	ABN96857
43	70.2	34.4	3732	19	AAV55040
44	68.6	33.6	1435	17	AAZ43709
45	62.8	30.8	2474	18	AAZ70840

ALIGNMENTS

RESULT 1

AAZ48862

ID AAZ48862 standard; cDNA; 1659 BP.

XX AAZ48862;

AC AAZ48862;

DT 24-MAR-2000 (first entry)

XX Human XIAP coding sequence.

DE Human XIAP coding sequence.

XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;

KW transforming growth factor-beta activated kinase 1; monocyte migration;

KW TAK1 binding protein 1; extracellular matrix protein production;

KW cell growth inhibitor; beta-amyloid protein deposition;

KW immunosuppression; Transforming growth factor-beta; ds.

XX Homo sapiens.

XX JP11326328-A.

XX 26-NOV-1999.

XX 13-MAY-1998; 98JP-0130378.

XX 13-MAY-1998; 98JP-0130378.

XX (MATS/) MATSUMOTO K.

XX WPI; 2000-078337/07.

XX P-PSDB; AAY59451.

XX Screening a substance which inhibits combination of the X-linked

PT

inhibitor of apoptosis protein

PT inhibitor of apoptosis protein -
XX
PS Disclosure: Page 28-30; 43pp; Japanese.

inhibitor of apoptosis protein -
Disclosure: Page 28-30; 43pp; Japanese.
This sequence encodes the human XIAP protein.
The invention relates to a method for screening a substance inhibiting the formation of a complex between XIAP and TAB1, in which X-linked inhibitor of apoptosis protein (XIAP), transforming growth factor-beta activated kinase 1 (TRAK1) binding protein 1 (TAB1) and a substance to be tested are contacted with each other and then the presence or formation of a complex between XIAP and TAB1 is detected. The substance can be used as a drug for extracellular matrix protein production enhancement, cell growth inhibition, monocyte migration, physiologically active substance induction, immunosuppression, and beta-amyloid protein deposition. A substance inhibiting the formation of a complex between TAB1 and XIAP as well as between XIAP and TRAF-beta (transforming growth factor-beta) type I and/or type II receptor is useful as a drug.

Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;

Query Match	100.0%;	Score 204;	DB 21;	Length 1659;
Best Local Similarity	100.0%;	Pred. No. 6.6e-59;		
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	Indels	0;		

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568	Db	GAAGAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCACCTACCCCAAGA	627
61	QY	GAGTTAGCAAGTCGTGGACTCTACTACACAGGATTTGGTGACCAAGTCAGTGCCTTTTGT	120
628	Db	GAGTTAGCAAGTCGTGGACTCTACTACACAGGATTTGGTGACCAAGTCAGTGCCTTTTGT	687
121	QY	TGTGGTGGAAAACTGAAAAATTTGGGAACCTTGTGATCGTGCTGGTCGAAACACACAGGGGA	180
688	Db	TGTGGTGGAAAACTGAAAAATTTGGGAACCTTGTGATCGTGCTGGTCGAAACACACAGGGGA	747
181	QY	CACCTTCCTAAATTCGCTCTTTTGT	204
748	Db	CACCTTCCTAAATTCGCTCTTTTGT	771

RESULT 2
AAT70836

ARI70836
ID AAT70836 standard; cDNA: 2540 BP.

AAT70836;

DT 02-SEP-1997 (first entry)

Human apoptosis inhibitor xiap cdna.

Apoptosis inhibitor; X-linked inhibitor of apoptosis protein; XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome; ischaemia; myocardial infarction; stroke; reperfusion injury; toxin-induced liver disease; gene therapy; diagnosis: ds.

OS Homo sapiens.

XX	Key	Location/Qualifiers
FH	CDS	34..1527
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FT		

PN WO9706255-A2.

XX
PD 20-FEB-1997.

05-AUG-1996: 96WO-TB01022-

22-DEC-1995: 95US-0576956

PR 04-AUG-1995; 9505-0311485.
XX

XX Baird S, Korneluk RG, Liston P, Mackenzie AE;
PI
XX
DR WPI; 1997-154262/14.
DR P-PSDE; AAW19581.

Nucleic acid encoding an inhibitor of apoptosis polypeptide - used to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection of susceptibility to apoptotic disease

PS Claim 12; Page 67-68; 219pp; English.

Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and hiap-2 genes (AA70836-41) respectively code for a new class of mammalian proteins (AAW19581-86) that are inhibitors of apoptosis (IAP). The xiap gene (for X-linked IAP gene) was isolated from a human fetal brain Zap1 cDNA library using an X-linked sequence tag site that shows strong homology with the conserved ring zinc finger domain of baculovirus CrpA and OpiA genes. The gene was assigned to chromosome Xq25 by FISH. IAP nucleic acids can be used to express IAP polypeptides in cells and animals to inhibit apoptosis, and as primers and probes to identify and isolate additional IAP genes, as well as in methods for treating diseases and disorders involving apoptosis (anti-apoptotic gene therapy).

Sequence 2540 BP: 781 A: 415 C: 570 G: 773 T: 1 other;

Query Match	100.0%	Score 204:	DB 18;	Length 2540;
Best Local Similarity	100.0%	Pred. No. 7.7e-59;		
Matches 204; Conservative	0;	Mismatches	0;	Indels 0;

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Db	520	GAGAAGAGCTAGATTAAGTGCCTTTGAGAACTGGCCAGAGACTATGCTCACCTTAACCCCAAGA	579
QY	61	GAGTTAGCAAGTGCCTGGAGCTCTACTACACAGGTATTGGTGACCAAGTGCAGTGCCTTTGT	120
Db	580	GAGTTAGCAAGTGCCTGGAGCTCTACTACACAGGTATTGGTGACCAAGTGCAGTGCCTTTGT	639
QY	121	TGTGGTGGAAACCTGAAAAATTTGGGAACCTTGTGATCGTGCCCTGGTTCAGAACACAGCGCA	180
Db	640	TGTGGTGGAAACCTGAAAAATTTGGGAACCTTGTGATCGTGCCCTGGTTCAGAACACAGCGCA	699
QY	181	CACCTTCCTCAATTGCCTCTTTGTT	204
Db	700	CACCTTCCTCAATTGCCTCTTTGTT	723

RESULT 3

AAA64901

ID AAA64901 standard; DNA; 2540 BP.

AAA64901;

DT 07-NOV-2000 (first entry)

DE Human X-linked inhibitor of apoptosis DNA.

KW x-linked inhibitor of apoptosis; XIAP; hIAP; MIHA; U45880;
 KW antisense; antiinflammatory; cytostatic; tumour; ds.
 KW

YY Homo sapiens.

XX	Key	Location/Qualifiers
FH	CDS	34..1527
FT		/+tag 3
FT		

FF V

PN US6087173-A.
v.v.

PD 11-JUL-2000.
yy

XX PR 09-SEP-1999; 99US-0392580.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Cowser LM, Ackermann EJ;
XX PR WPI: 2000-498201/44.
XX DR P-PSDB: AAY99985.
XX PT Antisense compound useful for research reagents, diagnostics,
XX PT prophylaxis and for treating disorders associated with x-linked
XX PT inhibitor of apoptosis, modulates expression of x-linked inhibitor of
XX PT apoptosis
XX XX
XX Example 13; Column 43-48; 33pp; English.
XX CC The present invention relates to antisense oligonucleotides designed to
XX CC inhibit expression of the human x-linked inhibitor of apoptosis. The
XX CC present sequence is the x-linked inhibitor of apoptosis DNA.
XX CC Modified phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are
XX CC more effective inhibitors than unmodified oligonucleotides. The
XX CC oligonucleotides may be used to inhibit x-linked inhibitor of apoptosis
XX CC expression in cells and tissues in vitro. The oligonucleotides are also
XX CC useful for treating animals or humans, prone to a disease associated
XX CC with x-linked inhibitor of apoptosis. The oligonucleotides may also be
XX CC used prophylactically to prevent infection, inflammation or tumour
XX CC formation.
XX XX
XX SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 other;
Query Match 100.0%; Score 204; DB 21; Length 2540;
Best Local Similarity 100.0%; Pred. No. 7.7e-59;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTACCTACACCAAGA 60
DB 570 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTACCTACACCAAGA 579
QY 61 GAGTTAGCAAGTGGGACTCTACTACACAGTATTGGTACCAAGTGCAGTCTTTTGT 120
DB 580 GAGTTAGCAAGTGGGACTCTACTACACAGTATTGGTACCAAGTGCAGTCTTTTGT 639
QY 121 TGTGTGGAAGAACTGAAATTTGGAACTTGTGATCGTCTGTCAGAACACAGGCGA 180
DB 640 TGTGTGGAAGAACTGAAATTTGGAACTTGTGATCGTCTGTCAGAACACAGGCGA 699
QY 181 CACTTTCCTAATTGCTTCTTTGTT 204
DB 700 CACTTTCCTAATTGCTTCTTTGTT 723
RESULT 4
ABK93869
ID ABK93869 standard; cDNA: 2540 BP.
XX AC ABK93869;
XX XX
XX DT 26-AUG-2002 (first entry)
XX DE Human cDNA encoding inhibitor of apoptosis, XIAP #1.
XX KW Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
XX KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
XX KW pancreatic cancer; embryonic development; viral pathogenesis;
XX KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
XX KW lupus erythematosus; herpes virus infection; pox virus infection;
XX KW adenovirus infection; proliferative disease.
XX OS
XX PN Homo sapiens.
XX PN WO200226968-A2.
XX XX

PD 04-APR-2002.
XX XX 27-SEP-2001; 2001WO-CA01379.
XX PF 28-SEP-2000; 2000US-0672717.
XX PR (UYOT-) UNIV OTTAWA.
XX PA (ABGE-) AEGERA THERAPEUTICS INC.
XX XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX WPI: 2002-479562/51.
XX DR P-PSDB: ABG65663.
XX PT Novel antisense inhibitor of apoptosis nucleic acid useful for
XX PT enhancing apoptosis in a cell, for treating cancer and other
XX PT proliferative diseases
XX PS Disclosure; Fig 1; 135pp; English.
XX CC The invention relates to an inhibitor of apoptosis (IAP) antisense
XX CC nucleic acid (I) that inhibits IAP biological activity, regardless of
XX CC length of the antisense nucleic acid, the IAP proteins may be mouse
XX CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
XX CC composition comprising a mammalian IAP antisense molecule and a method of
XX CC enhancing apoptosis in a cell, comprising administering a negative
XX CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
XX CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
XX CC mammal diagnosed with a proliferative disease. The method is useful for
XX CC treating a patient diagnosed with a proliferative disease like cancer.
XX CC The IAP antisense molecule is useful to treat, ameliorate, improve,
XX CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
XX CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
XX CC conditions where apoptosis is involved or implicated (e.g. embryonic
XX CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
XX CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
XX CC virus, pox virus and adenovirus). The present sequence is a human IAP
XX CC cDNA sequence.
XX XX
XX SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;
Query Match 100.0%; Score 204; DB 24; Length 2540;
Best Local Similarity 100.0%; Pred. No. 7.7e-59;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTACCTACACCAAGA 60
DB 570 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTACCTACACCAAGA 579
QY 61 GAGTTAGCAAGTGGGACTCTACTACACAGTATTGGTACCAAGTGCAGTCTTTTGT 120
DB 580 GAGTTAGCAAGTGGGACTCTACTACACAGTATTGGTACCAAGTGCAGTCTTTTGT 639
QY 121 TGTGTGGAAGAACTGAAATTTGGAACTTGTGATCGTCTGTCAGAACACAGGCGA 180
DB 640 TGTGTGGAAGAACTGAAATTTGGAACTTGTGATCGTCTGTCAGAACACAGGCGA 699
QY 181 CACTTTCCTAATTGCTTCTTTGTT 204
DB 700 CACTTTCCTAATTGCTTCTTTGTT 723
RESULT 5
ABK93875
ID ABK93875 standard; cDNA: 3000 BP.
XX AC ABK93875;
XX XX
XX DT 26-AUG-2002 (first entry)
XX DE Human cDNA encoding inhibitor of apoptosis, XIAP #2.
XX KW Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
XX KW

KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Homo sapiens.
 XX
 XX WO200226968-A2.
 XX
 XX 04-APR-2002.
 XX
 XX 27-SEP-2001; 2001WO-CA01379.
 XX
 XX 28-SEP-2000; 2000US-0672717.
 XX
 XX (UYOT-) UNIV OTTAWA.
 XX (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX
 XX WPI; 2002-479562/51.
 XX
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for
 XX enhancing apoptosis in a cell, for treating cancer and other
 XX proliferative diseases
 XX
 XX Example 2; Fig 15; 135pp; English.
 XX
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC cDNA sequence.
 XX
 SQ Sequence 3000 BP; 974 A; 452 C; 501 G; 973 T; 0 other;
 Query Match 100.0%; Score 204; DB 24; Length 3000;
 Best Local Similarity 100.0%; Pred. No. 8.2e-59;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTACCTACCCCAAGA 60
 DB 1176 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTACCTACCCCAAGA 1235
 QY 61 GAGTTAGCAAGTGGTGGACTCTACTACACAGGTATTGGTGCACCAAGTCAGTCTTTTGT 120
 DB 1236 GAGTTAGCAAGTGGTGGACTCTACTACACAGGTATTGGTGCACCAAGTCAGTCTTTTGT 1295
 QY 121 TGTGTGGAAACTGAAATAATGGGAACCTTGTGATCGTGCCTGTCAGAACACAGGCGA 180
 DB 1296 TGTGTGGAAACTGAAATAATGGGAACCTTGTGATCGTGCCTGTCAGAACACAGGCGA 1355
 QY 181 CACTTTCCTAATGCTCTCTTTTGT 204
 DB 1356 CACTTTCCTAATGCTCTCTTTTGT 1379
 RESULT 6
 AAV55038

ID AAV55038 standard; cDNA; 5232 BP.
 XX
 XX AAV55038;
 XX
 XX 13-NOV-1998 (first entry)
 XX
 XX Human XIAP coding sequence.
 XX
 XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.
 XX
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 XX CDS 34..1527
 XX /*tag= a
 XX /product= XIAP
 XX
 XX WO9835693-A2.
 XX
 XX 20-AUG-1998.
 XX
 XX 13-FEB-1998; 98WO-IB00781.
 XX
 XX 13-FEB-1997; 97US-0800929.
 XX
 XX (UYOT-) UNIV OTTAWA.
 XX
 XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
 XX Tsang B;
 XX
 XX WPI; 1998-467164/40.
 XX P-PSDB; AAW69294.
 XX
 XX Inducing apoptosis in proliferative mammalian cells with inhibitor
 XX of IAP or NAIP polypeptide - also methods for prognosis based on
 XX presence of IAP and NAIP, specifically applied to cancers involving
 XX p53 mutations
 XX
 XX Claim 13; Fig 1; 147pp; English.
 XX
 CC This sequence encodes the human XIAP protein, which is an inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver nasopharynx, thyroid, central nervous system, prostate, colon,
 CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis;
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors.
 XX
 SQ Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;
 Query Match 100.0%; Score 204; DB 19; Length 5232;
 Best Local Similarity 100.0%; Pred. No. 1e-58;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTACCTACCCCAAGA 60
 DB 520 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTACCTACCCCAAGA 579
 QY 61 GAGTTAGCAAGTGGTGGACTCTACTACACAGGTATTGGTGCACCAAGTCAGTCTTTTGT 120
 DB 580 GAGTTAGCAAGTGGTGGACTCTACTACACAGGTATTGGTGCACCAAGTCAGTCTTTTGT 639
 QY 121 TGTGTGGAAACTGAAATAATGGGAACCTTGTGATCGTGCCTGTCAGAACACAGGCGA 180

Db. 640 TGTGGTGGAAACTGAAATTTGGGAACCTTGTGATCGTGCCTGTGATGAGAACACAGCGGA 699

QY 181 CACTTTCCCTAATTCCTCTTTGTT 204
 |||||

Db 700 CACTTTCCCTAATTCCTCTTTGTT 723
 |||||

RESULT 7

AK99405

ID AAK99405 standard; DNA; 2404 BP.

XX AAK99405;

XX 27-JUN-2002 (first entry)

XX DNA of APP related human homologue hCP35211.

XX Neuroprotective; neurotropic; transgenic fly; Alzheimer's disease; Abeta;

KW amyloid precursor protein; tissue-specific expression control; human APP;

KW APP pathway modulator; gene therapy; gene; ds.

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS 692..1528

FT /*tag- a

FT /product= "Protein of human homologue hCP35211"

FT /note= "No start codon"

XX WO200226820-A2.

XX 04-APR-2002.

XX 01-OCT-2001; 2001WO-BP11345.

XX 29-SEP-2000; 2000US-236893P.

XX 14-JUN-2001; 2001US-298309P.

XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.

XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;

PI Reinhardt MWHM, Zusman S;

XX WPI; 2002-315796/35.

DR P-PSDB; AAO20511.

XX New transgenic fly, containing DNA encoding an Abeta portion of human

PT APP, useful for identifying agents which modulate the APP pathway and

PT which can be used to treat Alzheimer's disease -

XX Example 4; Page 111; 129pp; English.

XX The invention relates to a transgenic fly whose genome comprises DNA

CC encoding a polypeptide having the Abeta portion of human amyloid

CC precursor protein (APP), fused to a signal sequence. The DNA sequence

CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in

CC the specification. The DNA sequence is operably linked to a tissue-

CC specific expression control sequence. Expression of the sequence gives

CC the fly an altered phenotype. The purpose of the invention is for

CC identifying agents that inhibit or promote the expression and/or function

CC of genes or encoded polypeptides which modify the APP pathway. The agent

CC is a compound, triple helix DNA, antisense oligonucleotide, double

CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used

CC to treat conditions such as Alzheimer's disease. The agent can be used as

CC an APP pathway modulator or in gene therapy. This polynucleotide sequence

CC represents the DNA of the APP related human homologue hCP35211.

XX

SQ Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 other;

Query Match 94.6%; Score 193; DB 24; Length 2404;

Best Local Similarity 99.5%; Pred. No. 4.1e-55;

Matches 204; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60
 |||||

Db 520 GAAGAAGCTAGATTAAAGTCCTTTAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 579
 |||||

QY 61 GAGTTAGCAAGTCTGGACTCTACTACAGAGTATTGGTGACCAAGTGCAAGTCTTTTGT 120
 |||||

Db 580 GAGTTAGCAAGTCTGGACTCTACTACAGAGTATTGGTGACCAAGTGCAAGTCTTTTGT 639
 |||||

QY 121 TGTGGTGGAAACTGAAATTTGGGAACCTTGTGATCGTGCCTGTGATGAGAACACAGCGG 179
 |||||

Db 640 TGTGGTGGAAACTGAAATTTGGGAACCTTGTGATCGTGCCTGTGATGAGAACACAGCGG 699
 |||||

QY 180 ACACCTTTCTAATTCCTCTTTGTT 204
 |||||

Db 700 ACACCTTTCTAATTCCTCTTTGTT 724
 |||||

RESULT 8

AAT70839

ID AAT70839 standard; cDNA; 2100 BP.

XX AAT70839;

XX 02-SEP-1997 (first entry)

XX Mouse apoptosis inhibitor m-xiap cDNA.

DE Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;

XX M-Xiap; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;

KW Ischaemia; myocardial infarction; stroke;

KW reperfusion injury; toxin-induced liver disease; gene therapy;

KW diagnosis; ds.

XX Mus sp.

XX

FH Key Location/Qualifiers

FT CDS 127..1617

FT /*tag- a

XX WO9706255-A2.

XX 20-FEB-1997.

XX 05-AUG-1996; 96WO-IB01022.

XX 22-DEC-1995; 95US-0576956.

PR 04-AUG-1995; 95US-0511485.

XX (UYOT-) UNIV OTTAWA.

XX Baird S, Korneluk RG, Liston P, Mackenzie AE;

PI WPI; 1997-154262/14.

DR P-PSDB; AAMI9584.

XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used

PT to inhibit apoptosis in e.g. HIV or AIDS patients; and for detection

PT of susceptibility to apoptotic disease

XX Claim 11; Page 78-79; 219pp; English.

XX Human xiap, hlap-1 and hlap-2 genes, and murine xiap, hlap-1 and

CC hlap-2 genes (AAT70836-41) respectively code for a new class of

CC mammalian proteins (AAMI9581-86) that are inhibitors of apoptosis

CC (IAP). The murine xiap gene (for X-linked IAP gene) sequence was

CC constructed from 12 overlapping clones isolated from a mouse

CC embryo lambda-gt11 cDNA library and from a mouse FIX II genomic

CC library using human xiap cDNA as probe. IAP nucleic acids can be

CC used to express IAP polypeptides in cells and animals to inhibit

CC apoptosis, and as primers and probes to identify and isolate

CC additional IAP genes, as well as in methods for treating diseases

CC and disorders involving apoptosis (anti-apoptotic gene therapy).

XX SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;

Query Match 84.3%; Score 172; DB 18; Length 2100;
Best Local Similarity 90.2%; Pred. No. 5.1e-48;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCTTTCAGAACTGGCCAGACTATGCTCACTAACCCCAAGA 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 613 GAAGAAGCCAGATTGAAGTCAATTTTCAGAACTGGCCGGACTATGCTCATTTAACCCCAAGA 672
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTGTGACCAAGTGCAGTGCCTTTTGT 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 673 GAGTTAGTCTAGTGTGGCTCTACTACACAGGGCTGATGATCAAGTGCATGCTTTTGT 732
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 TGTGTTGAAACACTGAAAAATTTGGGAACCTTGTGATCGTGGCTGCTCAGAACACACAGGCGA 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 733 TGTGGGGAAAACTGAAAAATTTGGGAACCTTGTGATCGTGGCTGCTCAGAACACACAGGCGA 792
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 181 CACTTTCCTAATTGCTCTTTTGT 204
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 793 CACTTTCCTAATTGCTCTTTTGT 816
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 9
ABK93872
ID ABK93872 standard; cDNA; 2100 BP.
XX AC ABK93872;
XX XX
DT 26-AUG-2002 (first entry)
XX XX
DE Mouse cDNA encoding inhibitor of apoptosis, XIAP.
XX XX
KW Mouse; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW pancreatic cancer; embryonic development; viral pathogenesis;
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW lupus erythematosus; herpes virus infection; pox virus infection;
KW adenovirus infection; proliferative disease.
XX XX
OS Mus sp.
XX OS
XX WO200226968-A2.
XX PN
XX PD 04-APR-2002.
XX XX
XX 27-SEP-2001; 2001WO-CA01379.
XX XX
XX 28-SEP-2000; 2000US-067217.
XX XX
XX (UYOT-) UNIV OTTAWA.
XX PA (AEGE-) AEGERA THERAPEUTICS INC.
XX PA
XX XX
PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX XX
DR WPI; 2002-479562/51.
XX P-PSDB; ABG65666.
XX XX
PT Novel antisense inhibitor of apoptosis nucleic acid useful for
PT enhancing apoptosis in a cell, for treating cancer and other
PT proliferative diseases -
XX XX
XX Disclosure; Fig 4; 135pp; English.
XX XX
CC The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (1) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse
CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a

PT p53 mutations
 XX Claim 13; Fig 4; 147pp; English.
 PS This sequence encodes the mouse XIAP protein, which is an inhibitor of
 XX apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, especially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver, gasopharynx, thyroid, central nervous system, prostate, colon,
 CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors.
 XX Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 other;
 SQ Query Match 84.3%; Score 172; DB 19; Length 2691;
 Best Local Similarity 90.2%; Pred. No. 5.7e-48;
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAGTCTTTCAGAACTGGCCAGACTATGCTCACCCTAACCCCAAGA 60
 DB 1158 GAAGAAGCCAGATTAAGTCTTTCAGAACTGGCCAGACTATGCTCACCCTAACCCCAAGA 1217
 QY 61 GAGTTAGCAAGTCTGAGCTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 120
 DB 1218 GAGTTAGCTAGTCTGGCTCTACTACACAGGGCTGATGATCAATGCTCAATGCTTTGT 1277
 QY 121 TGTGTGGAAACTGAAATTTGGGAACCTTGTGATCGTGCCCTGGTCAGAACACAGCGGA 180
 DB 1278 TGTGGGGGAAACTGAAATTTGGGAACCTTGTGATCGTGCCCTGGTCAGAACACAGCGGA 1337
 QY 181 CACTTCTCAATGCTCTTTTGT 204
 DB 1338 CACTTCTCAATGCTCTTTTGT 1361

RESULT 11
 AAT72710
 ID AAT72710 standard; DNA; 1988 BP.
 XX AAT72710;
 AC AAT72710;
 DT 16-SEP-1997 (first entry)
 XX Mouse inhibitor of apoptosis protein homologue MIHA DNA.
 XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
 KW degenerative disease; infectious disease; autoimmune disease;
 KW cancer; gene therapy; diagnosis; ss.
 XX Mus musculus.
 XX Key Location/Qualifiers
 FT CDS 212..1702
 FT /*tag= a
 XX W09723501-A1.
 XX 03-JUL-1997.
 XX 20-DEC-1996; 96WO-AU00827.
 XX 22-DEC-1995; 95AU-0007275.
 XX (AMRA-) AMRAD OPERATIONS, PTY LTD.
 XX

PI Vaux DL;
 XX WPI: 1997-350966/32.
 DR P-PSDB; AAW19745.
 XX Isolated protein homologues of viral inhibitors of apoptosis - used
 PT to modulate apoptosis for treatment of degenerative, infectious or
 PT autoimmune diseases and cancer
 XX Claim 24; Page 44-47; 136pp; English.
 XX An isolated nucleic acid molecule (AAT72710) codes for mammalian IAP
 CC homologue A (MIHA) (AAW19745), a murine homologue of baculovirus
 CC inhibitor of apoptosis protein (IAP). It was isolated from a mouse
 CC liver cDNA library on the basis of homology to Orgyia pseudotsuguta
 CC polydrosis virus IAP BIR and RING finger amino acid motifs.
 CC Animal IAP homologue nucleic acids (see also AAT72711-17) can be used
 CC to produce polypeptides useful in methods for modulating apoptosis
 CC in animal cells, specifically for treatment, by inhibition, of
 CC degenerative and infectious disease or, by promotion, of cancer and
 CC autoimmune disease, and can be used for gene therapy of these
 CC diseases.
 XX Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 other;
 SQ Query Match 83.5%; Score 170.4; DB 18; Length 1988;
 Best Local Similarity 89.7%; Pred. No. 1.8e-47;
 Matches 183; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAGTCTTTCAGAACTGGCCAGACTATGCTCACCCTAACCCCAAGA 60
 DB 698 GAAGAAGCCAGATTAAGTCTTTCAGAACTGGCCAGACTATGCTCACCCTAACCCCAAGA 757
 QY 61 GAGTTAGCAAGTCTGAGCTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 120
 DB 758 GAGTTAGCTAGTCTGGCTCTACTACACAGGGCTGATGATCAATGCTCAATGCTTTGT 817
 QY 121 TGTGTGGGAAACTGAAATTTGGGAACCTTGTGATCGTGCCCTGGTCAGAACACAGCGGA 180
 DB 818 TGTGGGGGAAACTGAAATTTGGGAACCTTGTGATCGTGCCCTGGTCAGAACACAGCGGA 877
 QY 181 CACTTCTCAATGCTCTTTTGT 204
 DB 878 CACTTCTCAATGCTCTTTTGT 901

RESULT 12
 ABR14677
 ID ABR14677 standard; cDNA; 1758 BP.
 XX ABR14677;
 AC ABR14677;
 XX 08-MAY-2002 (first entry)
 XX Human inhibitor of apoptosis protein 7 (IAPL7) cDNA.
 DE Human; gene; inhibitor of apoptosis 7; IAPL7; cytostatic;
 KW antiapoptotic; IAP; apoptosis; antibody; V-Rel; NF-kappaB;
 KW chromosome 19; vaccine; gene therapy; hyperproliferative disease;
 KW cancer; transgenic animal; ss.
 XX Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 286..1680
 FT /*tag= a
 FT /product= "IAPL7 protein"
 FT /partial
 FT /note= "No start codon shown"
 XX W0200210381-A1.
 XX 07-FEB-2002.
 XX

XX 18-JUL-2001; 2001WO-EP08287.
PF
XX 28-JUL-2000; 2000EP-0116452.
PR
XX (MERE) MERCK PATENT GMBH.
PA
XX Hentsch B;
PI
XX WPI: 2002-188741/24.
DR P-PSDB; AAU75747.
XX
XX New inhibitor of apoptosis proteins and polynucleotides useful in
PT vaccines for inducing an immune response against hyperproliferative
PT diseases e.g. cancer
PT
XX
XX
PS Claim 5; Page 33-35; 41pp; English.
XX
CC This invention relates to the nucleic acid and protein sequences of a
CC novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences
CC have homology to the IAP (inhibitors of apoptosis) gene family which
CC are thought to inhibit proteins by regulating the anti-apoptotic
CC activity of the V-Rel and Nr-kappaB family of transcription factors.
CC The gene for IAPL7 is located on human chromosome 19. The nucleic acids
CC of the invention are useful for screening to identify compounds that
CC stimulate or inhibit the function or level of IAPL7, where the
CC identified compounds are useful for treating hyper-proliferative
CC diseases such as cancer. The protein sequences may also be used to
CC identify membrane bound or soluble receptors of IAPL7 by standard
CC receptor binding techniques. Nucleic acids encoding IAPL7, may be used
CC as hybridisation probes for cDNA and genomic DNA, or as primers for
CC nucleic acid amplification reaction and the primers and probes may also
CC be used to isolate full-length cDNAs and genomic clones encoding IAPL7.
CC The nucleic acid sequences are useful as diagnostic reagents for
CC diagnosing a disease or a susceptibility to a disease by detecting
CC mutations in the associated gene. The nucleic acid sequence is useful
CC for chromosome localisation and tissue expression studies and is also
CC useful for producing transgenic animals. The IAPL7 protein sequence may
CC also be used to generate an anti-IAPL7 antibody which is useful in
CC screening methods for detecting the effect of added compounds on the
CC production of mRNA and protein in cells. The sequences of the invention
CC are also useful as vaccines for inducing an immunological response in a
CC mammal. The present sequence represents the cDNA encoding the human
CC inhibitor of apoptosis 7 (IAP7) protein of the invention.
XX
SQ Sequence 1758 BP; 488 A; 371 C; 470 G; 429 T; 0 other;
Query Match 81.2%; Score 165.6; DB 24; Length 1758;
Best Local Similarity 88.2%; Pred. No. 7, 1e-46;
Matches 180; Conservative 0; Mismatches 24; Indels 0; Gaps 0;
QY 1 GAAGAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60
DB 673 GAAGAGCTAGATTACAGTCGTTTTCACAACTGGCCAGCTCTGCCACCTTGACCGGAGA 732
QY 61 GAGTAGCAAGTGTGAGCTCTACTACACAGGTATTGGTGACACAGTGCAGTCTTCT 120
DB 733 GAGTGGCCAGCTGTGGCTGTACTACAGGCACCTGATGACCAAGTGCGAGTCTCTGT 792
QY 121 TGTGTGGAACAACTGAAATTTGGAACTTGTGATCGTCTGCTGCTGCAACACAGGCGA 180
DB 793 TGTGGCGGAACTGAAAACTGGGAACCTGTGATCGTCTGCTGCTGCAACACAGGAGA 852
QY 181 CACTTTCCTAAATGCTCTTTGTT 204
DB 853 CATTTTCCTAAATGCTCTTTATT 876
RESULT 13
ABK13197
ID ABK13197 standard; DNA; 1559 BP.
XX
AC ABK13197;

XX 23-APR-2002 (first entry)
DT
XX Human testes specific inhibitor of apoptosis (TIAP) gene.
DE
XX TIAP; apoptosis; testes specific inhibitor of apoptosis; gene;
KW human; ds; apoptotic; cytostatic; anti-infertility; contraceptive;
KW chromosome 12q22-23; transgenic animal; antibody; immunogen;
KW testicular cell; testicular cancer; cancer; male infertility;
KW male birth control; XIAP.
XX
OS Homo sapiens.
XX
XX Key Location/Qualifiers
PH 791..1501
FT CDS /*tag= a
FT /product= "TIAP protein"
XX
XX US6331412-B1.
PN
XX 18-DEC-2001.
PD
XX 29-JAN-1999; 99US-0239867.
PF
XX 29-JAN-1998; 98US-073001P.
PR
XX (UYOT-) UNIV OTTAWA.
PA
XX Korneluk RG, Lagace M;
PI
XX WPI: 2002-105275/14.
DR P-PSDB; AAU75066.
XX
PT Nucleic acids encoding a testis specific apoptosis inhibitor protein
PT (TIAP) useful for treating testicular cancers, cancers in
PT non-testicular tissues, male infertility, and for achieving male birth
PT control
XX
XX Claim 2; Fig 4A; 29pp; English.
XX
PS This invention relates to a novel isolated nucleic acid molecule
CC encoding a TIAP polypeptide (testes-specific inhibitor of apoptosis)
CC protein. This gene is a homologue of the X-linked XIAP gene and is
CC located on chromosome 12q22-23. The nucleotide and protein sequences of
CC the invention and vectors containing these sequences may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate TIAP expression. Additionally, the nucleotide sequence may
CC be used to express the TIAP protein by recombinant methods. Conversely,
CC antisense nucleic acid molecules may be administered to down-regulate
CC TIAP expression. The nucleotide sequence, may also be used to design DNA
CC probes for diagnostic assays (e.g. polymerase chain reactions (PCR)) to
CC detect and quantitate the presence of similar nucleic acid sequences in
CC samples, to identify patients who may be in need of restorative therapy.
CC Through the production of transgenic animals and cells, the sequences
CC may also be used to study the expression and function of TIAP proteins
CC and their role in metabolism. The TIAP polypeptides may be used to
CC produce antibodies against TIAP and may be used to identify modulators
CC (agonists and antagonists) of TIAP expression and activity. An anti-TIAP
CC antibody or antagonist may also be used to down-regulate TIAP expression
CC and activity. The reagents may be used in this way for the treatment of
CC excessive or insufficient apoptosis, particularly in testicular cells.
CC In particular they are useful in diagnosing and treating testicular
CC cancers, cancers in non-testicular tissues, male infertility, and for
CC achieving male birth control. The present sequence represents the
CC human TIAP gene sequence of the invention.
XX
SQ Sequence 1559 BP; 465 A; 309 C; 396 G; 387 T; 2 other; 1
Query Match 80.4%; Score 164; DB 24; Length 1559;
Best Local Similarity 87.7%; Pred. No. 2, 4e-45;
Matches 179; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 GAAGAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60

XX (USSH.) US DEPT HEALTH & HUMAN SERVICES.
PA Duckett C, Mir SS;
PI
XX
XX WPI: 2001-258135/26.
DR P-PSDB; NAE00365.
XX
XX Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
PT transforming growth factor beta receptor modulating activity, and the
PT nucleic acids that encode them, useful for treating, e.g. diabetes and
PT multiple sclerosis -
XX
XX Claim 18; Page 94-98; 108pp; English.
PS
XX
XX The present sequence is human inhibitor of apoptosis (IAP)-like protein-2
CC (ILP-2) cDNA. The ILP-2 gene is located on chromosome 19q13.3-q13.4.
CC ILP-2 comprises a single amino-terminal domain known as baculovirus IAP
CC repeat (BIR), followed by a spacer region and a carboxy-terminal ring
CC finger domain. It interacts with transforming growth factor beta
CC receptor (TGFbetaR) and modulates TGFbetaR activity. It also potentially
CC inhibits apoptosis induced by overexpression of Bax or by Caspase-9 and
CC Apaf-1. It also activates c-Jun N-terminal kinase (JNK) activity. ILP-2
CC is used in the area of genetic testing for predisposition to diseases,
CC such as cone-rod retinal dystrophy-2, retinitis pigmentosa,
CC glutaricaciduria, T-cell acute lymphoblastic leukaemia, colorectal cancer
CC and hyperferritinemia-cataract syndrome owing to an ILP-2 deletion or
CC mutation. The ILP is also used in the treatment of diseases associated
CC with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,
CC diabetes and multiple sclerosis and neurodegenerative diseases including
CC retinal degeneration. The ILP-2 gene is also used in gene therapy for
CC treating patients suffering from ILP-2 gene deletions or mutations.
XX
XX SQ Sequence 4993 BP; 1526 A; 973 C; 1196 G; 1297 T; 1 other;
Query Match 80.4%; Score 164; DB 22; Length 4993;
Best Local Similarity 87.7%; Pred. No. 3.7e-45;
Matches 179; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 GAAGAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60
Db 1777 GAAGAAGCTAGATAACAGTCGGTTTCAAACTGGCCAGCCTCTGCCCACTTGACCCCGAGA 1836
QY 61 GAGTTAGCAAGTCTGCTACTACTACACAGGATTTGGTGACCAAGTCAGTGCTTTTGT 120
Db 1837 GAGCTGGCCAGTGTGGGCTGTACTACACAGGCACTGATGACCAAGTCAGTGCTTCTGT 1896
QY 121 TGTGGTGGAAACTGAAAAATTTGGGAACCTTGTGATCGTGCTGTGTCAGAACACACAGGCA 180
Db 1897 TGTGGCGGAAACTGAAAACTGGGAACCTTGTGATCGTGCTGTGTCAGAACACACAGGCA 1956
QY 181 CACTTTCCTAATTGCTTCTTTGT 204
Db 1957 CATTTCCTAATTGCTTCTTTATT 1980

Search completed: April 15, 2003, 21:45:25
Job time : 140.354 secs

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:16:42 ; Search time 25.6771 Seconds
(without alignments)
2436.494 Million cell updates/sec

Title: US-09-654-743-46
Perfect score: 204
Sequence: 1 gaagaagctagattaaagtc.....ttcctaattgcttttgggt 204

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
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2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*
3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*
5: /cgn2_6/ptodata/1/ina/PTOUS_COMB.seq:*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	100.0	1588	4	US-09-239-867-3
2	204	100.0	2540	2	US-08-511-485-3
3	204	100.0	2540	3	US-09-392-580-1
4	204	100.0	5232	3	US-09-212-971-3
5	204	100.0	5232	3	US-08-800-929A-3
6	204	100.0	5232	4	US-09-617-053A-3
7	172	84.3	2100	2	US-08-511-485-9
8	172	84.3	2691	3	US-09-212-971-9
9	172	84.3	2691	3	US-08-800-929A-9
10	172	84.3	2691	4	US-09-617-053A-9
11	164	80.4	1559	4	US-09-239-867-1
12	84.6	41.5	2601	4	US-08-569-749-3
13	84.6	41.5	2601	5	PCT-US96-12860-3
14	84.6	41.5	2676	2	US-08-511-485-5
15	84.6	41.5	3076	2	US-09-205-144-1
16	84.6	41.5	6669	3	US-09-212-971-5
17	84.6	41.5	6669	3	US-08-800-929A-5
18	84.6	41.5	6669	4	US-09-617-053A-5
19	74.4	36.5	2862	4	US-08-569-749-13
20	74.4	36.5	2862	5	PCT-US96-12860-13
21	74.4	36.5	3151	3	US-09-212-971-13
22	74.4	36.5	3151	3	US-08-800-929A-13
23	74.4	36.5	3151	4	US-09-617-053A-13
24	70.2	34.4	2580	2	US-08-511-485-7
25	70.2	34.4	2589	4	US-08-569-749-1
26	70.2	34.4	2589	5	PCT-US96-12860-1
27	70.2	34.4	3532	2	US-09-205-204-1

28	70.2	34.4	3732	3	US-09-212-971-7	Sequence 7, Appl
29	70.2	34.4	3732	3	US-08-800-929A-7	Sequence 7, Appl
30	70.2	34.4	3732	4	US-09-617-053A-7	Sequence 7, Appl
31	68.6	33.6	1435	5	PCT-US95-0522A-1	Sequence 1, Appl
32	62.8	30.8	2676	3	US-09-212-971-11	Sequence 11, Appl
33	62.8	30.8	2676	3	US-08-800-929A-11	Sequence 11, Appl
34	62.8	30.8	2676	4	US-09-617-053A-11	Sequence 11, Appl
35	58.2	28.5	5502	3	US-08-836-134-1	Sequence 1, Appl
36	58.2	28.5	5502	4	US-09-493-784-1	Sequence 1, Appl
37	41.2	20.2	711	3	US-09-121-979-3	Sequence 3, Appl
38	41.2	20.2	711	4	US-09-332-319-3	Sequence 3, Appl
39	38.8	19.0	176373	3	US-09-128-155-17	Sequence 17, Appl
40	38.4	18.8	152331	3	US-09-128-155-16	Sequence 16, Appl
41	28	13.7	28	2	US-08-859-998-1232	Sequence 1232, Ap
42	28	13.7	28	4	US-09-225-928-1232	Sequence 1232, Ap
43	28	13.7	1287	4	US-09-028-274A-16	Sequence 16, Appl
44	27.8	13.6	2000	4	US-09-553-889A-1	Sequence 1, Appl
45	27.6	13.5	758	4	US-09-712-016-28	Sequence 28, Appl

ALIGNMENTS

RESULT 1
US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-239-867-3

Query Match	100.0%;	Score 204;	DB 4;	Length 1588;
Best Local Similarity	100.0%;	Pred. No. 8.6e-62;		
Matches 204;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA	60	
Db	520	GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA	579	
QY	61	GAGTTAGCAAGTGTGGAGCTCTACTACACAGGTATTTGGTGACCAAGTCAGTCTTTTGT	120	
Db	580	GAGTTAGCAAGTGTGGAGCTCTACTACACAGGTATTTGGTGACCAAGTCAGTCTTTTGT	639	
QY	121	TGTGTTGGAAGTGAATAATTTGGAACTTTGATCGTCCGTCAGAACACAGCGGA	180	
Db	640	TGTGTTGGAAGTGAATAATTTGGAACTTTGATCGTCCGTCAGAACACAGCGGA	699	
QY	181	CACCTTCCTAATTCCTTTTGT	204	
Db	700	CACCTTCCTAATTCCTTTTGT	723	

RESULT 2
US-08-511-485-3
; Sequence 3, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen

;; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
;; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
;; NUMBER OF SEQUENCES: 38
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Fish & Richardson P.C.
;; STREET: 225 Franklin Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110-2804
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/511.485
;; FILING DATE: 04-AUG-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T.
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 07540/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2540 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: DNA (genomic)
US-08-511-485-3

Query Match 100.0%; Score 204; DB 2; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1e-61;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60
|||||
DB 520 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579

QY 61 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 120
|||||
DB 580 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 639

QY 121 TGTGGTGAAGAACTGAAAAATTGGAACTTGTGATCGCTGGTCAGACACAGGCGA 180
|||||
DB 640 TGTGGTGAAGAACTGAAAAATTGGAACTTGTGATCGCTGGTCAGACACAGGCGA 699

QY 181 CACTTTCCTAATTCCTCTTTGTT 204
|||||
DB 700 CACTTTCCTAATTCCTCTTTGTT 723

RESULT 3
US-09-392-580-1
; Sequence 1, Application US/09392580
; Patent No. 6087173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSIO
; FILE REFERENCE: RFS-0072
; CURRENT APPLICATION NUMBER: US/09/392.580
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2540
; TYPE: DNA

;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: (34)..(1527)
US-09-392-580-1

Query Match 100.0%; Score 204; DB 3; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1e-61;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60
|||||
DB 520 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579

QY 61 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 120
|||||
DB 580 GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 639

QY 121 TGTGGTGAAGAACTGAAAAATTGGAACTTGTGATCGCTGGTCAGACACAGGCGA 180
|||||
DB 640 TGTGGTGAAGAACTGAAAAATTGGAACTTGTGATCGCTGGTCAGACACAGGCGA 699

QY 181 CACTTTCCTAATTCCTCTTTGTT 204
|||||
DB 700 CACTTTCCTAATTCCTCTTTGTT 723

RESULT 4
US-09-212-971-3
; Sequence 3, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212.971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017.354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030.590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800.929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (4623)..(4623)
; OTHER INFORMATION: n can be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (4622)..(4622)
; OTHER INFORMATION: n can be any nucleotide
US-09-212-971-3

Query Match 100.0%; Score 204; DB 3; Length 5232;
Best Local Similarity 100.0%; Pred. No. 1.4e-61;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60
|||||
DB 520 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579

QY 61 GAGTACCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 120
|||||
Db 580 GAGTACCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 639
QY 121 TGTGGTGGAAACTGAAAAATTTGGAACTTGTGATGTCGCTGGTGACCAACACAGCGCA 180
|||||
Db 640 TGTGGTGGAAACTGAAAAATTTGGAACTTGTGATGTCGCTGGTGACCAACACAGCGCA 699
QY 181 CACTTTCCTAATTCCTCTTTGTT 204
|||||
Db 700 CACTTTCCTAATTCCTCTTTGTT 723

RESULT 5

US-08-800-929A-3
; Sequence 3, Application US/08800929A
; Patent No. 6133437

GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110

COMPUTER READABLE FORM:

; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1..5232
; OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.

Query Match 100.0%; Score 204; DB 3; Length 5232;
Best Local Similarity 100.0%; Pred. No. 1.4e-61;

US-08-800-929A-3

Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAAGAAGCTAGATTAAAGTCTCTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60
|||||
Db 520 GAAGAAGCTAGATTAAAGTCTCTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579
QY 61 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 120
|||||
Db 580 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 639
QY 121 TGTGGTGGAAACTGAAAAATTTGGAACTTGTGATGTCGCTGGTGACCAACACAGCGCA 180
|||||
Db 640 TGTGGTGGAAACTGAAAAATTTGGAACTTGTGATGTCGCTGGTGACCAACACAGCGCA 699
QY 181 CACTTTCCTAATTCCTCTTTGTT 204
|||||
Db 700 CACTTTCCTAATTCCTCTTTGTT 723

RESULT 6

US-09-617-053A-3
; Sequence 3, Application US/09617053A
; Patent No. 6300492

GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: variation

LOCATION: (4623)...(4623)

OTHER INFORMATION: n can be any nucleotide

NAME/KEY: variation

LOCATION: (4622)...(4622)

OTHER INFORMATION: n can be any nucleotide

US-09-617-053A-3

Query Match 100.0%; Score 204; DB 4; Length 5232;
Best Local Similarity 100.0%; Pred. No. 1.4e-61;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCTCTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 60
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Db 520 GAAGAAGCTAGATTAAAGTCTCTTCAGAACTGGCCAGACTATGCTACCTAACCCCAAGA 579
QY 61 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 120
|||||
Db 580 GAGTTAGCAAGTCTGGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTGT 639
QY 121 TGTGGTGGAAACTGAAAAATTTGGAACTTGTGATGTCGCTGGTGACCAACACAGCGCA 180
|||||
Db 640 TGTGGTGGAAACTGAAAAATTTGGAACTTGTGATGTCGCTGGTGACCAACACAGCGCA 699
QY 181 CACTTTCCTAATTCCTCTTTGTT 204
|||||
Db 700 CACTTTCCTAATTCCTCTTTGTT 723

```
RESULT 7
US-08-511-485-9
; Sequence 9, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511.485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match      84.3%; Score 172; DB 2; Length 2100;
Best Local Similarity 90.2%; Pred. No. 1.5e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCGAGACTATGCTCAGCTTAACCCCAAGA 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 613 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGAGACTATGCTCATTTAACCCCAAGA 672
QY 61 GAGTTAGCAAGTCGGACTCTACTACACAGTATTGTGTGACCAAGTCAGTGCTTTTGT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 673 GAGTTAGTAGTCGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 732
QY 121 TGTGTGGAAGAACTGAAATTTGGAACTTTGTGATCGTCTGCTCAGAACACAGGCGA 180
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 733 TGTGGGGGAAACTGAAATTTGGAACTTTGTGATCGTCTGCTCAGAACACAGGAGA 792
QY 181 CACTTTCCTAATTGCTTTTGT 204
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 793 CACTTCCCAATTGCTTTTGT 816

RESULT 8
US-09-212-971-9
; Sequence 9, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
```

APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-800-929A-9

Query Match 84.3%; Score 172; DB 3; Length 2691;
Best Local Similarity 90.2%; Pred. No. 1.6e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCGAGACTATGCTCACCTAACCCCAAGA 60
DB 1158 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGAGACTATGCTCATTTAACCCCAAGA 1217
QY 61 GAGTTAGCAAGTGTGGGCTCTACTACACAGGTATTGGTGACCAAGTGCAGTGCTTTTGT 120
DB 1218 GAGTTAGTGTGGGCTCTACTACACAGGGGCTGATCAAGTGAATGCTTTTGT 1277
QY 121 TGTGGTGGAAACTGAAATTTGGAACTTGTGATCGTGGTGCAGAACACAGGCGA 180
DB 1278 TGTGGGGGAAACTGAAATTTGGAACTTGTGATCGTGGTGCAGAACACAGGAGGA 1337
QY 181 CACTTTCCCTAATGCTTTTGT 204
DB 1338 CACTTTCCCAATGCTTTTGT 1361

RESULT 10
US-09-617-053A-9
Sequence 9, Application US/09617053A
Patent No. 6300492
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 2691
TYPE: DNA
ORGANISM: Mus musculus
US-09-617-053A-9

Query Match 84.3%; Score 172; DB 4; Length 2691;
Best Local Similarity 90.2%; Pred. No. 1.6e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCGAGACTATGCTCACCTAACCCCAAGA 60
DB 1158 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGAGACTATGCTCATTTAACCCCAAGA 1217
QY 61 GAGTTAGCAAGTGTGGGCTCTACTACACAGGTATTGGTGACCAAGTGCAGTGCTTTTGT 120
DB 1218 GAGTTAGTGTGGGCTCTACTACACAGGGGCTGATCAAGTGAATGCTTTTGT 1277
QY 121 TGTGGTGGAAACTGAAATTTGGAACTTGTGATCGTGGTGCAGAACACAGGCGA 180
DB 1278 TGTGGGGGAAACTGAAATTTGGAACTTGTGATCGTGGTGCAGAACACAGGAGGA 1337
QY 181 CACTTTCCCTAATGCTTTTGT 204
DB 1338 CACTTTCCCAATGCTTTTGT 1361

RESULT 11
US-09-239-867-1
Sequence 1, Application US/09239867
Patent No. 6331412
GENERAL INFORMATION:
APPLICANT: Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
TITLE OF INVENTION: MALE FERTILITY
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/09/239,867
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,001
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 1559
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(1559)
OTHER INFORMATION: n = A,T,C or G
US-09-239-867-1

Query Match 80.4%; Score 164; DB 4; Length 1559;
Best Local Similarity 87.7%; Pred. No. 8.1e-48;
Matches 179; Conservative 0; Mismatches 25; Indels 0; Gaps 0;
QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCGAGACTATGCTCACCTAACCCCAAGA 60
DB 494 GAAGAAGCTAGATAACAGTCGTTTCACAACTGGCCGAGCTTGCCTGACCTGACCCGAGA 553
QY 61 GAGTTAGCAAGTGTGGGCTCTACTACACAGGTATTGGTGACCAAGTGCAGTGCTTTTGT 120
DB 554 GAGCTGGCCGAGTGTGGGCTGTACTACACAGGCACTGTGACCAAGTGCAGTGCTTCTGT 613
QY 121 TGTGGTGGAAACTGAAATTTGGAACTTGTGATCGTGGTGCAGAACACAGGCGA 180
DB 614 TGTGGGGGAAACTGAAATTTGGAACTTGTGATCGTGGTGCAGAACACAGGAGGA 673
QY 181 CACTTTCCCTAATGCTTTTGT 204
DB 674 CATTTCCTAATGCTTCTTATT 697

RESULT 12
US-08-569-749-3
Sequence 3, Application US/08569749
Patent No. 6187557
GENERAL INFORMATION:
APPLICANT: Rothe, Mike


```
QY 61 GAGTTAGCAAGTCGCGACTCTACTACAGAGTATTGGTGACCAAGTCAGTGCCTTTTGT 120
|||||
Db 580 GAGTTAGCAAGTCGCGACTCTACTACAGAGTATTGGTGACCAAGTCAGTGCCTTTTGT 639
QY 121 TGTGTGGAAGAACTGAAATTTGGAACTTGTATCGTGCCTGTGTCAGAACACAGGCGA 180
|||||
Db 640 TGTGTGGAAGAACTGAAATTTGGAACTTGTATCGTGCCTGTGTCAGAACACAGGCGA 699
QY 181 CACTTTCTTAATGCTTCTTTGTT 204
|||||
Db 700 CACTTTCTTAATGCTTCTTTGTT 723

RESULT 2
US-09-974-592-3
; Sequence 3, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: Variation
; LOCATION: 4623
; OTHER INFORMATION: n can be any nucleotide
; NAME/KEY: Variation
; LOCATION: 4622
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-3

Query Match 100.0%; Score 204; DB 10; Length 5232;
Best Local Similarity 100.0%; Pred. No. 2.8e-62;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTACCTACCCCAAGA 60
|||||
Db 520 GAAGAAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTACCTACCCCAAGA 579
QY 61 GAGTTAGCAAGTCGCGACTCTACTACAGAGTATTGGTGACCAAGTCAGTGCCTTTTGT 120
|||||
Db 580 GAGTTAGCAAGTCGCGACTCTACTACAGAGTATTGGTGACCAAGTCAGTGCCTTTTGT 639
QY 121 TGTGTGGAAGAACTGAAATTTGGAACTTGTATCGTGCCTGTGTCAGAACACAGGCGA 180
|||||
Db 640 TGTGTGGAAGAACTGAAATTTGGAACTTGTATCGTGCCTGTGTCAGAACACAGGCGA 699
QY 181 CACTTTCTTAATGCTTCTTTGTT 204
|||||
Db 700 CACTTTCTTAATGCTTCTTTGTT 723
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RESULT 3
US-09-964-899-38
; Sequence 38, Application US/09964899
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; Patent No. US2002017446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo Sapien
US-09-964-899-38

Query Match 94.6%; Score 193; DB 9; Length 2404;
Best Local Similarity 99.5%; Pred. No. 1.7e-58;
Matches 204; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTACCTACCCCAAGA 60
|||||
Db 520 GAAGAAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTACCTACCCCAAGA 579
QY 61 GAGTTAGCAAGTCGCGACTCTACTACAGAGTATTGGTGACCAAGTCAGTGCCTTTTGT 120
|||||
Db 580 GAGTTAGCAAGTCGCGACTCTACTACAGAGTATTGGTGACCAAGTCAGTGCCTTTTGT 639
QY 121 TGTGTGGAAGAACTGAAATTTGGAACTTGTATCGTGCCTGTGTCAGAACACAGGCG 179
|||||
Db 640 TGTGTGGAAGAACTGAAATTTGGAACTTGTATCGTGCCTGTGTCAGAACACAGGCG 699
QY 180 ACATTTCTTAATGCTTCTTTGTT 204
|||||
Db 700 ACATTTCTTAATGCTTCTTTGTT 724

RESULT 4
US-09-201-936-9
; Sequence 9, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9

Query Match 84.3%; Score 172; DB 9; Length 2100;
Best Local Similarity 90.2%; Pred. No. 4.7e-51;
```



```
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60
Db 613 GAAGAGCCGAGATTGAAGTCATTTCAGAACTGGCCGAGTATGCTCATTTAACCCCAAGA 672

QY 61 GAGTTAGCAAGTCTGGAGCTCTACTACACAGGATTTGTTGACCAAGTGCAGTCTTTTGT 120
Db 673 GAGTTAGCTAGTCTGGCCCTCTACTACACAGGGGCTGATGATCAAGTGCAGTCTTTTGT 732

QY 121 TGTGGTGGAAACTGAAAAATTGGGAACCTTGTGATCGTCCCTGGTCAGAACACAGCGCA 180
Db 733 TGTGGGGGAAACTGAAAAATTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGCGAGA 792

QY 181 CACTTTCCTAAATTCCTCTTTTGT 204
Db 793 CACTTTCCTAAATTCCTCTTTTGT 816

RESULT 5
US-09-974-592-9
; Sequence 9, Application US/09974592
; Patent No. US2002012012IA1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0.
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-974-592-9

Query Match 84.3%; Score 172; DB 10; Length 2691;
Best Local Similarity 90.2%; Pred. No. 5.2e-51;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60
Db 1158 GAAGAGCCGAGATTGAAGTCATTTCAGAACTGGCCGAGTATGCTCATTTAACCCCAAGA 1217

QY 61 GAGTTAGCAAGTCTGGAGCTCTACTACACAGGATTTGTTGACCAAGTGCAGTCTTTTGT 120
Db 1218 GAGTTAGCTAGTCTGGCCCTCTACTACACAGGGGCTGATGATCAAGTGCAGTCTTTTGT 1277

QY 121 TGTGGTGGAAACTGAAAAATTGGGAACCTTGTGATCGTCCCTGGTCAGAACACAGCGCA 180
Db 1278 TGTGGGGGAAACTGAAAAATTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGCGAGA 1337

QY 181 CACTTTCCTAAATTCCTCTTTTGT 204
Db 1338 CACTTTCCTAAATTCCTCTTTTGT 1361

RESULT 6
US-09-201-936-5
; Sequence 5, Application US/09201936
; Publication No. US20020187946A1
```

```
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 5
; LENGTH: 2676
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2470)...(2470)
; OTHER INFORMATION: N may be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2476)...(2476)
; OTHER INFORMATION: N may be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2483)...(2483)
; OTHER INFORMATION: N may be any nucleotide
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2602)...(2602)
; OTHER INFORMATION: N may be any nucleotide
; US-09-201-936-5

Query Match 41.5%; Score 84.6; DB 9; Length 2676;
Best Local Similarity 67.0%; Pred. No. 6.4e-20;
Matches 136; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 1 GAAGAGCTAGATTAAAGTCCTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60
Db 693 GAAATGCCAGATTACTTACTTTTCAGACATGGCCA---TTGACTTTTCTGTCGCCAACA 749

QY 61 GAGTTAGCAAGTCTGGAGCTCTACTACACAGGATTTGTTGACCAAGTGCAGTCTTTTGT 120
Db 750 GATCGGCAGCAGCAGCGCTTTTACTACATAGACCTGGAGACAGAGTGGCTTGTGCTGCC 809

QY 121 TGTGGTGGAAACTGAAAAATTGGGAACCTTGTGATCGTCCCTGGTCAGAACACAGCGCA 180
Db 810 TGTGGTGGAAATTTGACCAATTTGGGAACCGAGGATTAATGCTATGTCAGAACACCTGAGA 869

QY 181 CACTTTCCTAAATTCCTCTTTTGT 203
Db 870 CATTTCCTAAATTCCTCTTTTGT 892

RESULT 7
US-09-954-531-16
; Sequence 16, Application US/09954531
; Patent No. US20020165180A1
; GENERAL INFORMATION:
; APPLICANT: Weaver, Zoe
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-77
; CURRENT APPLICATION NUMBER: US/09/954,531
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; CURRENT FILING DATE: 2002-05-02
; PRIOR APPLICATION NUMBER: US/60/233,133
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,009
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,034
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,509
; PRIOR FILING DATE: 2000-09-22
; PRIOR APPLICATION NUMBER: US/60/234,567
; PRIOR FILING DATE: 2000-09-22
; NUMBER OF SEQ ID NOS: 1392
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 16
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-554-531-16

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Query Match	41.5%	Score 84.6;	DB 9;	Length 3076;
Best Local Similarity	67.0%;	Pred. No. 6.8e-20;		
Matches 136;	Conservative	0;	Mismatches 64;	Indels 3; Gaps 1;
QY 1	GAGGAAGCTAGATTAAGTCTCTTTGACAACTGGCCAGACTATGCTCACCTAACCCCAAGA	60		
Db 1229	GAAATGCCAGATTACTTTTACACATATGGCA---TTGACTTTTCTGTGCGCAACA	1285		
QY 61	GAGTTAGCAAGTGTGTGACTCTTACTACACAGGTATTTGGTGACCAGTGCAGTGTCTTTGT	120		
Db 1286	GATCTGGCAAAAGCAGGCTTTTACTACATATGACCTGGAGACAGAGTGGCTTGCTTTGCC	1345		
QY 121	TGTGGTGGAAACATGAAAAATTTGGAACTTGTATCTGCTGCTGTCAGACACAGGCGGA	180		
Db 1346	TGTGGTGGAAATTTGACCAATTTGGGAACCGAAGGATATGCTATGTCAAGAACCTTGAGA	1405		
QY 181	CACTTTCCCTAATTCCTTTCTTTGT	203		
Db 1406	CATTTCGCCAAATGCCATTAT	1428		

RESULT 8
US-09-954-456-1635
; Sequence 1635, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Candi
; TITLE OF INVENTION: Sets
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0

```

; SEQ ID NO 1635
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1635

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Query Match	41.58;	Score	84.6;	DB	10;	Length	3076;
Best Local Similarity	67.08;	Pred. No.	6.8e-20;				
Matches	136;	Conservative	0;	Mismatches	64;	Indels	3; Gaps
Qy	1	GAACAAGCTACATAAAGTCCTTTTCAGAACTGGCCAGACACTATGCTCACCTTAACCCCAAGA	60				
Db	1229	GAAATGCCAGATTACITACTTTTCAGACATGGCCA---TTGACTTTTCTGTGCGCAACA	1285				
Qy	61	GAGTTAGCAAGTGTGGACTCTACTACACAGGTATTGTGTGACCAGTGCAGTGTCTTTGT	120				
Db	1286	GATCTGSCAAAGCAGGCGTTTCTACTATAGGACCTGGAGACAGAGTGGCTGTCTTTGCC	1345				
Qy	121	TGTCGTGGAAACCTGAAAAATTTGSGAACCTTTGTATCTGTCTGTGTGACAGACACAGGGGA	180				
Db	1346	TGTCGTGGAAAAATTGAGCAATTTGSGAACCGAAGGATATGCTATGTCAGACACACCTGAGA	1405				
Qy	181	CACTTTCCTAATTCTTCCTTTGT	203				
Db	1406	CATTTTCCCAAAATGCCATTAT	1428				

RESULT 9

```

US-09-974-592-5
; Sequence 5, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
; TITLE OF INVENTION: NAPI FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6669
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (3677)...(3951)
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-5

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	Query Match	41.5%	Score 84.6;	DB 10;	Length 6669;
	Best Local Similarity	67.0%;	Pred. No. 9.4e-20;		
	Matches 136;	Conservative 0;	Mismatches 64;	Indels 3;	Gaps 1
Qy	1 GAAGAACTAGATTAAAGTCCTTTTCCAGAACTGGCCAGACTATGCTCACCATAACCCCAGA	60			
Dd	4725 GAAAATGCCAGATTACTTTCTTTTCCAGACATGCSCA---TTGACHTTTTCTGTGCGCAACA	4781			
Qy	61 GAGTTAGCAAGTGCTGGGAAGTCTACTACACAGGTAATGGTGACCAAGTGCAGTGCTTTTCT	120			
Dd	4782 SATCTGGCACAGCAGGCTTTTACTACATAGGACCTGGAGACAGTAGTGCTTTGGCC	4841			
Qy	121 TGTGCTGGAAAACTGAAAATTTGGAAACCTTGTGATGCTGCTGTGACAAACACAGCGCA	180			

Db 4842 TGTGGTGAATAATGACCAATGGACCAAGGATAATGCTATGTCTAGACACCTGAGA 4901
Qy 181 CACTTCTCAATGCTCTTTGT 203
Db 4902 CATTTTCCCAATGCCCATTTAT 4924

RESULT 10
US-09-796-692-3493/c
; Sequence 3493, Application US/09796692
; Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796.692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3493
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-3493

Query Match 38.4%; Score 78.4; DB 9; Length 240;
Best Local Similarity 68.1%; Pred. No. 3.7e-18;
Matches 109; Conservative 0; Mismatches 51; Indels 0; Gaps 0;
Qy 44 CTCACCTAACCCCAAGAGAGTAGCAAGTGTGGACTCTACTACACAGGTATGTGACC 103
Db 233 CTTTCTCTCGCCCAACAGATCTGCAAAAGCAGGCTTTTACTACATAGGACCTGGAGACA 174
Qy 104 AAGTGCAGTCTTTTGTGTGGTGAACCTGAAATTTGGAACTTGTGATCTGCT 163
Db 173 GAGTGGCTTGTCTTCCCTGTGGTGAATTTGAGCAATTTGGCAATGGCAAGGATAATGCTA 114
Qy 164 GGTCAACACAGGCGACACTTCTTAATGCTCTTTGT 203
Db 113 TGTCAACACCTGAGACATTTTCCCAATGCCCATTTAT 74

RESULT 11
US-09-796-692-6687
; Sequence 6687, Application US/09796692

Publication No. US20020198362A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THE
; TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
; FILE REFERENCE: 2077.001200
; CURRENT APPLICATION NUMBER: US/09/796.692
; CURRENT FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: 60/186,126
; PRIOR FILING DATE: 2000-03-01
; PRIOR APPLICATION NUMBER: 60/190,479
; PRIOR FILING DATE: 2000-03-17
; PRIOR APPLICATION NUMBER: 60/200,545
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: 60/200,303
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,779
; PRIOR FILING DATE: 2000-04-28
; PRIOR APPLICATION NUMBER: 60/200,999
; PRIOR FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 60/202,084
; PRIOR FILING DATE: 2000-05-04
; PRIOR APPLICATION NUMBER: 60/206,201
; PRIOR FILING DATE: 2000-05-22
; PRIOR APPLICATION NUMBER: 60/218,950
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 60/222,903
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: 60/223,416
; PRIOR FILING DATE: 2000-08-04
; PRIOR APPLICATION NUMBER: 60/223,378
; PRIOR FILING DATE: 2000-08-07
; NUMBER OF SEQ ID NOS: 9597
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 6687
; LENGTH: 240
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-6687

Query Match 37.6%; Score 76.8; DB 9; Length 240;
Best Local Similarity 67.5%; Pred. No. 1.4e-17;
Matches 108; Conservative 0; Mismatches 52; Indels 0; Gaps 0;
Qy 44 CTCACCTAACCCCAAGAGAGTAGCAAGTGTGGACTCTACTACACAGGTATGTGACC 103
Db 8 CTTTCTCTCGCCCAACAGATCTGCAAAAGCAGGCTTTTACTACATAGGACCTGGAGACA 67
Qy 104 AAGTGCAGTCTTTTGTGTGGTGAACCTGAAATTTGGAACTTGTGATCTGCT 163
Db 68 GAGTGGCTTGTCTTCCCTGTGGTGAATTTGGCAATTTGGCAATGGCAAGGATAATGCTA 127
Qy 164 GGTCAACACAGGCGACACTTCTTAATGCTCTTTGT 203
Db 128 TGTCAACACCTGAGACATTTTCCCAATGCCCATTTAT 167
RESULT 12
US-09-974-592-13
; Sequence 13, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE

```

; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 3151
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-974-592-13

Query Match      36.5%; Score 74.4; DB 10; Length 3151;
Best Local Similarity 62.2%; Pred. No. 2.9e-16;
Matches 117; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 7 GCTAGATTAAGTCCTTTGAGAAGTGGCCAGACATGCTCACCTAACCCCAAGAGAGTTA 66
   ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1568 GCTCAGTGTAGGACATTTCTTACTGGCCACTAGTGTCTGTTTCAGCCGACGAGCTT 1627
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 67 GCAAGTCGTGACCTACTACACAGGATTTGGTCACCAAGTGCAGTGTGTTTGTGCGT 126
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1628 GCAAGTCGTGAGTCTTATTAGCTGGATGCGCAATGATGATGTCAGAGTGTCTTTGTTGTGAT 1687
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 127 GGAAACCTGAAAAATGGGAACCTTGTCGTGCTCGTGCAGAACACAGCGACACACTTT 186
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1688 GGTGGCTTGAGATGTTGGGAACCTGGAGATGACCCCTGGATAGAACACGCCCAATGGTTT 1747
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 187 CCTAATTG 194
   |||||
Db 1748 CCAAGGTG 1755
   |||||

RESULT 13
US-09-201-936-41
; Sequence 41, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-41

```

Qy	67	GCAAGTCTGGGACTCTACTACACAGTATTGGTGACCAAGTGCAGT	GCTTTTGTGGT	126
Db	929	GCAAGTCTGGGATTCCTATTACGTGGATGCAATGATGATGTC	CAAGTGCCTTTGTGTGAT	988
Qy	127	GGAAGACTGAAGAAATGGGAACCTTGTGATCGTCTGTCAGAACAC	GAGCGACACTT	186
Db	989	GGTGGCTTGAGATGTTGGGAACCTGGAGATGACCCCTGGATAGAAC	ACGCCCAATGGTTT	1048
Qy	187	CCTAATTG	194	
Db	1049	CCAAGGTG	1056	
<p>RESULT 14</p> <p>US-09-778-927A-21</p> <p>; Sequence 21, Application US/09778927A</p> <p>; Patent No. US20020068342A1</p> <p>; GENERAL INFORMATION:</p> <p>; APPLICANT: KHOSRAVI, Rami et al.</p> <p>; TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL</p> <p>; TITLE OF INVENTION: VARIANTS OF ALTERNATIVE SPLICING</p> <p>; FILE REFERENCE: 2786-0160P</p> <p>; CURRENT APPLICATION NUMBER: US/09/778,927A</p> <p>; CURRENT FILING DATE: 2001-02-08</p> <p>; PRIOR APPLICATION NUMBER: IL 134453</p> <p>; PRIOR FILING DATE: 2000-02-09</p> <p>; PRIOR APPLICATION NUMBER: IL135341</p> <p>; PRIOR FILING DATE: 2000-03-29</p> <p>; NUMBER OF SEQ ID NOS: 81</p> <p>; SOFTWARE: Patent In Ver. 2.1</p> <p>; SEQ ID NO 21</p> <p>; LENGTH: 2291</p> <p>; TYPE: DNA</p> <p>; ORGANISM: Homo sapiens</p> <p>; FEATURE:</p> <p>; NAME/KEY: misc_feature</p> <p>; LOCATION: (1)..(2291)</p> <p>; OTHER INFORMATION: n = a,c,g,t any unknown or other</p> <p>US-09-778-927A-21</p>				

FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 2580
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (2412)...(2412)
OTHER INFORMATION: N may be any nucleotide
US-09-201-936-7

Query Match 34.4% Score 70.2; DB 9; Length 2580;
Best Local Similarity 62.6% Pred. No. 8.4e-15;
Matches 127; Conservative 0; Mismatches 73; Indels 3; Gaps 1;
Qy 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCGAGACTATGCTCACCCTAACCCCAAGA 60
Db 787 GAAGAAGCCAGATTCTTACCTACCATATGTGGCCA---TTAACTTTTGTGTACCATCA 843
Qy 61 GAGTTAGCAAGTCTGGACTACTACACAGTATTGGTGACCAAGTCAGTGTCTTTGT 120
Db 844 GAATGGCARGAGCTGGTGTATATATAGGACCTGGAGATAGGGTAGCCCTGCTTTGCC 903
Qy 121 TGTGTGGAAGAACTGAAAATTTGGAACTTGTGATCGTCTGCTGCTCAGAACACACAGGCGA 180
Db 904 TGTGTGGGAGCTCAGTAACCTGGGACCAAGGATGATGCTATGTCAGACACCGGAGG 963
Qy 181 CACTTTCCTAATTCCTTTGT 203
Db 964 CATTTCCCAACTGTCCATTTT 986

Search completed: April 16, 2003, 01:02:27
Job time : 54.0521 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:12:47 ; Search time 976.083 Seconds
(without alignments)
3384.833 Million cell updates/sec

Title: US-09-654-743-46
Perfect score: 204
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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6: em_estpl:*
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8: em_htc:*
9: gb_est1:*
10: gb_est2:*
11: gb_htc:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	171	83.8	436	9	AI326613 mm83el2.y
4	163	79.9	375	9	AA097958 mm83el2.y
5	149	73.0	1020	13	BM554544 AGENCOURT
6	123.8	60.7	1130	13	BM553272 AGENCOURT

7	104.4	51.2	742	13	BI829221
8	84.6	41.5	557	9	AI051610
9	84.6	41.5	886	14	BQ652590
10	79.8	39.1	768	13	BM423292
11	79.2	38.8	593	13	BJ096099
12	78.2	38.3	567	13	BI961039
13	76.6	37.5	512	13	BI326908
14	75.6	37.1	459	13	BM446366
15	74.2	36.4	959	13	BM458775
16	72	35.3	298	12	BF016190
17	71.2	34.9	673	9	AL640649
18	70.2	34.4	401	12	BF095673
19	70.2	34.4	422	10	AW898626
20	70.2	34.4	889	14	BO720079
21	70.2	34.4	895	14	BQ884287
22	69.6	34.1	286	9	AA473594
23	68.8	33.7	450	12	BG729302
24	68.8	33.7	595	9	AI558531
25	68.6	33.6	649	10	AW949508
26	68.2	33.4	590	10	BE268377
27	68.2	33.4	837	12	BG743309
28	66.4	32.5	681	12	BF611032
29	66.2	32.5	851	13	BI253303
30	66.2	32.5	896	14	BO439248
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32	63.2	31.0	592	13	BJ059822
33	63.2	31.0	936	14	C81977
34	60.2	29.5	441	13	BM312708
35	60.2	29.5	563	9	AA702174
36	60.2	29.5	652	10	AV704923
37	60	29.4	953	17	CNS04211
38	59.4	29.1	395	9	AI552965
39	58.2	28.5	354	9	AA354707
40	57	27.9	302	14	R83677
41	57	27.9	341	10	AW375598
42	57	27.9	354	10	AW375594
43	57	27.9	402	10	AW846507
44	57	27.9	531	10	AW375599
45	57	27.9	532	10	AW846425

ALIGNMENTS

RESULT 1
BG502660

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

BG502660 822 bp mRNA linear EST 27-MAR-2001
602549490F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4657102 5',
mRNA sequence.
BG502660.1 GI:13464177
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 822)
NIH-MGC: http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgabbs@mail.nih.gov
Tissue Procurement: ARCC
CDNA Library Preparation: CLONETECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM1449 row: c column: 23
High quality sequence stop: 670.

FEATURES

source

Location/Qualifiers
1..822

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4637102"
/clone_lib="NIH_MGC_61"
/tissue_type="embryonal carcinoma"
/lab_host="DH10B (T1 phage-resistant)"
/notes="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
Site_2: SfiI (ggccattatggcc);
Double-stranded cDNA was prepared from cell line RNA. 5'
and 3' adaptors were used in cloning as follows: 5'
adaptor sequence: 5'-CACGGCATTATGGCC-3' and 3' adaptor
sequence: 5'-ATTCTAGAGCGCGGCGGACATG-DT(30)BN-3'
(Where B = A, C, G, or T). Average
insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
contained inserts by PCR. This library was enriched for
full-length clones and was constructed by Clontech
Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
Library."
BASE COUNT 236 a 161 c 201 g 222 t 2 others
ORIGIN

Query Match 100.0%; Score 204; DB 12; Length 822;
Best Local Similarity 100.0%; Pred. No. 2.le-59;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60
DB 337 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 396
QY 61 GAGTTAGCAAGTCTGGACTCTACTACACAGGATTGGTGACCAAGTGCAGTGTCTTTGT 120
DB 397 GAGTTAGCAAGTCTGGACTCTACTACACAGGATTGGTGACCAAGTGCAGTGTCTTTGT 456
QY 121 TGTGGTGGAAACTGAAATTTGGAACTTTGTGATCGTCCCTGGTGACAAACACAGCGGA 180
DB 457 TGTGGTGGAAACTGAAATTTGGAACTTTGTGATCGTCCCTGGTGACAAACACAGCGGA 516
QY 181 CACTTCTCTAATTCCTCTTTGT 204
DB 517 CACTTCTCTAATTCCTCTTTGT 540

RESULT 2
BM459898 1041 bp mRNA linear EST 05-FEB-2002
LOCUS ACENOCOURT_6422054 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5532247
DEFINITION 5', mRNA sequence.
ACCESSION BM459898
VERSION BM459898.1 GI:18508938
KEYWORDS EST.
SOURCE Human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1041)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: L1AM12215 row: d column: 08
High quality sequence stop: 567.
Location/Qualifiers
1. .1041
/organism="Homo sapiens"
/db_xref="taxon:9606"

```

```

/clone="IMAGE:5532247"
/clone_lib="NIH_MGC_71"
/tissue_type="leiomyosarcoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: uterus; Vector: pCMVSPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 2.1 kb.
BASE COUNT 297 a 208 c 266 g 269 t 1 others
ORIGIN

Query Match 88.5%; Score 180.6; DB 13; Length 1041;
Best Local Similarity 92.6%; Pred. No. 3e-51;
Matches 189; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60
DB 553 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 612
QY 61 GAGTTAGCAAGTCTGGACTCTACTACACAGGATTGGTGACCAAGTGCAGTGTCTTTGT 120
DB 613 GAGTTAGCAAGTCTGGACTCTACTACACAGGATTGGTGACCAAGTGCAGTGTCTTTGT 672
QY 121 TGTGGTGGAAACTGAAATTTGGAACTTTGTGATCGTCCCTGGTGACAAACACAGCGGA 180
DB 673 TGTGGTGGAAACTGAAATTTGGAACTTTGTGATCGTCCCTGGTGACAAACACAGCGGA 732
QY 181 CACTTCTCTAATTCCTCTTTGT 204
DB 733 CACTTCTCTAATTCCTCTTTGT 756

RESULT 3
AI326613 436 bp mRNA linear EST 23-DEC-1998
LOCUS mn3e12.y1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
DEFINITION IMAGE:550702 5' similar to SW:TAPEX_MOUSE Q60989 X-LINKED INHIBITOR
OF APOPTOSIS PROTEIN ;, mRNA sequence.
ACCESSION AI326613
VERSION AI326613.1 GI:4061042
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 436)
AUTHORS Maria,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geiseli,S., Kucaba,T., Lacy,M., Ie,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:331494
This read is a RESEQUENCE of a previously sequenced mouse clone
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: -40RP from Gibco
High quality sequence stop: 417.
Location/Qualifiers
1. .436
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:550702"
/clone_lib="Stratagene mouse Tcell 937311"

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FEATURES
source

```

/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
EcOri; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGGAG
3' -3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3'"

BASE COUNT      119 a      92 c      108 g      116 t      1 others
ORIGIN

Query Match      83.8%; Score 171; DB 9; Length 436;
Best Local Similarity 89.7%; Pred. No. 4.1e-48;
Matches 183; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCACCCTAACCCCAAGA 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGAGCTATGCTCATTTAACCCCAAGA 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GAGTTAGCAAGTCGCGGACTCTACTACACAGGTATTGGTGACCAAGTCAGTGCATTTTGT 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GAGTTAGCTAGTCGCGGCTCTACTACACAGGGCTGATGATCAAGTGCATTTTGT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 TGTGTGGAAGAACTGAAATTTGGAACTTGTGATCGTGCCTGCTGCAACACACAGGCGA 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TGTGGGGGAAACTGAAATTTGGAACTTGTGATCGTGCCTGCTGCAACACACAGGAGA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 CACTTTCCTAATGCTTCTTGT 204
      ||||| ||||| ||||| |||||
Db 361 CACTTTCCTAATGCTTCTTGT 384

RESULT 4
AA097958
LOCUS
DEFINITION
mn83el2.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
IMAGE:550702 5' similar to TR:G1145261 G1145261 MIHA. ;, mRNA
sequence.
ACCESSION
AA097958
VERSION
AA097958.1 GI:1643511
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 375)
Maier,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T.,
Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M.,
Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B.,
Theisinger,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and
Waterston,R.
The WashU-HHMI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
WashU-HHMI Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
MGI:331494
Possible reversed clone: similarity on wrong strand
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 191.
Location/Qualifiers
1..375
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:550702"
/clone_lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"

/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site_1:
EcOri; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGGAG
3' -3' adaptor sequence: 5' CTCGAGTCTTTTCTTTTCTTTT 3'"

BASE COUNT      109 a      86 c      89 g      91 t
ORIGIN

Query Match      79.9%; Score 163; DB 9; Length 375;
Best Local Similarity 89.7%; Pred. No. 2.3e-45;
Matches 175; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCACCCTAACCCCAAGA 60
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGAGCTATGCTCATTTAACCCCAAGA 240
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 61 GAGTTAGCAAGTCGCGGACTCTACTACACAGGTATTGGTGACCAAGTCAGTGCATTTTGT 120
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 241 GAGTTAGCTAGTCGCGGCTCTACTACACAGGGCTGATGATCAAGTGCATTTTGT 300
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 121 TGTGTGGAAGAACTGAAATTTGGAACTTGTGATCGTGCCTGCTGCAACACACAGGCGA 180
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 301 TGTGGGGGAAACTGAAATTTGGAACTTGTGATCGTGCCTGCTGCAACACACAGGAGA 360
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 CACTTTCCTAATGCT 195
      ||||| ||||| ||||| |||||
Db 361 CACTTTCCTAATGCT 375

RESULT 5
BM554544
LOCUS
DEFINITION
AGENCOURT_6546864 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5742590
5', mRNA sequence.
ACCESSION
BM554544
VERSION
BM554544.1 GI:18794228
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1020)
NIH-MGC http://mgi.mgi.mcgill.ca/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12760 row: p column: 15
High quality sequence stop: 730.
Location/Qualifiers
1..1020
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5742590"
/clone_lib="NIH_MGC_119"
/tissue_type="medulla"
/lab_host="DH10B"
/note="Organ: brain; Vector: pCMV-Sport6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source normal medulla from
anonymous male age 27. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.3kb, insert size range
0.9-3 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber

FEATURES
Source

```



```
Query Match      60.7%; Score 123.8; DB 13; Length 1130;
Best Local Similarity 84.8%; Pred. No. 1.5e-31;
Matches 173; Conservative 0; Mismatches 28; Indels 3;
```

BEST LOCAL SIMILARITY 84.8%; PRED. NO. 1.3E-31;
Matches 173; Conservative 0; Mismatches 28; Indels 3; Gaps 3;

1 GAAGGAGCTAGATTTAAAGTCTCTTTTCAGAAATGGCCAGACATATGCTCACCTTAACCCCA
776 GAAGGAGCTAGATTAACAGTCGTTTTCACAACTGGCAGCCCTGTGCCCTTTGACCCCCCA

61 GAGTATGCAAGTGCTGGACTCTACTACACAGGTATTGTCGACCAAGTGCACTGCTTTTGT
!!! | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
836 GAGCTGGCCAGTGCTGGGCTGTACTACACAGGCACCTGATGACC-AGTGCAGTGCTTCTGT

121 TGTGGTGGAAACTGAAAAATTGGGAACCTTGTCATCGTCCCTGGTCAAGAACACAGCGA 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
895 TGTTGCCGAAAACCTG-AAAACCTGGGAACCTGGTGCATCGTCCCTGGTCAAGAACACAGSAGA 953

181 CACTTTCCTAATTGCTTCTTTGT 204
||| ||| ||| ||| ||| |||
954 CA-TTTTCTAATGCCCTCTTTATT 976

RESULT 7

B29221
UCS
BI829221
742 bp'
mRNA linear EST 04-OCT-2001
603079537F1 NIH_MGC_119 Homo sapiens cDNA clone IMAGE:5171408 5', mRNA sequence

CESSION
 B1829221
 VERSION
 B1829221.1
 GI:15940771
 EST.
 KEYWORDS

SOURCE
ORGANISM
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi
Mammalia; Eutheria; Primates; Catarrhini. Hominoidea. Homo

REFERENCE
1 (bases 1 to 742)
NIH-MGC <http://mgc.ncl.nih.gov/>.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE

Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.

found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
 Plate: LLAM11426 row: 1 column: 09

FEATURES	High quality sequence stop: 700.
Location/Qualifiers	
1. .742	
source	

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5171408"
/clone_lib="NIH_MGC_119"

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```
/tissue_type="medulla"  
/lab_host="DH10B"  
/note="Organ: brain; vector: pCMV-SPORT6; site_1: NOTI
```

anonymous male age 27. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.3 kb. Insert size range 0.5-2.5 kb. **Site_2:** EcoRV (destroyed); RNA source normal medulla

0.9-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 013. N

SE COUNT
IGIN

Query Match	51.2%;	Score 104.4;	DB 13;	Length 742;
Best Local Similarity	85.0%;	Pred. No. 6.5e-25;		
Matches 175; Conservative	0;	Mismatches 26;	Indels 5;	Gaps

1 GAAGAAGCTAGATTA - AAGTCCTTTCAGAACT - GGCCAGACTATGC - TCACCTAACCCCA 57

|||||
Db 503 GAAGAGCTAGATTACAACTGCTTTCACAACTGGCCAGCCCTCTGGCCACTTGAACCCG 562
QY 58 AGAGAGTTAGCAAGTCTGGACTCTACTACACAGGTA-TTGTGGACCAAGTGCAGTGCTT 116
|||||
Db 563 AGAGAGCTGGCAGTCTGGCTGTACTACACAGGCACTTGATGACCAAGTGCAGTGCTT 622
QY 117 TTGTGTGTGGAAACCTGAAATTTGGAACTTGTGATCGTGGCTGTGACAGACACA- 175
|||||
Db 623 CTGTGTGGCGGAAACTGAAACTTGGGAACCTGTGTGATCGTGGCTGTGACAGACAC 682
QY 176 GCGACACTTCTCTAATGCTCTTT 201
|||||
Db 683 GGAGACATTTCTAATGCTCTTT 708
RESULT 8
LOCUS AI051610/c 557 bp mRNA linear EST 10-JUL-1998
DEFINITION oz02c09.x1 Soares fetal_liver_spleen.INFLS.S1 Homo sapiens cDNA
clone IMAGE:1674160 3' similar to SW:1AFL_HUMAN Q13489 INHIBITOR OF
APOPTOSIS PROTEIN 1 ;, mRNA sequence.
ACCESSION AI051610
VERSION AI051610.1 GI:3307144
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 557)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40ml3 fwd. Et from Amersham
High quality sequence stop: 436.
FEATURES
Location/Qualifiers
1..557
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1674160"
/clone_lib="Soares_fetal_liver_spleen.INFLS.S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subcloned version of the original Soares fetal
liver spleen INFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5',
AAGTGAAGAAATTAATTAAGATCTTTTCTTTTCTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."
BASE COUNT 162 a 101 c 120 g 174 t
ORIGIN
Query Match 41.5%; Score 84.6; DB 9; Length 557;
Best Local Similarity 67.0%; Pred. No. 4.1e-18;
Matches 136; Conservative 0; Mismatches 64; Indels 3; Gaps 1;
QY 1 GAAGAGCTAGATTAAAGTCTTTCAGAACTGGCCAGCACTATGCTCACTAACCCCAAGA 60
|||||
Db 396 GAAATGCCAGATTACTTACTTCTTTCAGACATGGCCA---TTGACTTTTCTGTGCGCAACA 340
QY 61 GAGTTAGCAAGTCTGGACTTACTACACAGGTAATGCTGACCAAGTGCAGTGCTTTTGT 120
|||||

Db 339 GATCTGGCAAAAGCAGGCTTTTACTACATAGGACCTGGAGACAGAGTGGCTTGTGCTTGC 280
QY 121 TGTGTGGGAAAACTGAAAAATTTGGAACTTGTGATCGTGGCTGGTGCAGAAACACAGGCGA 180
|||||
Db 279 TGTGTGGGAAAAATTTGAGCAATTTGGAACTGGAGGATAATGCTATGTCAGAACACCTGAGA 220
QY 181 CACTTTCCTAATTTGCTTCTTTGT 203
|||||
Db 219 CATTTCCTCAATGCTTCTTTAT 197
RESULT 9
LOCUS BQ652590 886 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT_8287942 NIH_MGC_100 Homo sapiens
cDNA clone IMAGE:6298025
5', mRNA sequence.
ACCESSION BQ652590
VERSION BQ652590.1 GI:21776762
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 886)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CGAP (Stanford)
cDNA Library Preparation: Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LCM2508 row: g column: 18
High quality sequence stop: 638.
FEATURES
Location/Qualifiers
1..886
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6298025"
/clone_lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: liver; Vector: pOB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into EcoRI/XhoI sites using the following 5' adaptor:
GGCACCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."
BASE COUNT 255 a 193 c 186 g 250 t 2 others
ORIGIN
Query Match 41.5%; Score 84.6; DB 14; Length 886;
Best Local Similarity 67.0%; Pred. No. 5.2e-18;
Matches 136; Conservative 0; Mismatches 64; Indels 3; Gaps 1;
QY 1 GAAGAGCTAGATTAAAGTCTTTCAGAACTGGCCAGCACTATGCTCACTAACCCCAAGA 60
|||||
Db 239 GAAATGCCAGATTACTTACTTTCAGACATGGCCA---TTGACTTTTCTGTGCGCAACA 295
QY 61 GAGTTAGCAAGTCTGGACTTACTACACAGGTAATGCTGACCAAGTGCAGTGCTTTTGT 120
|||||
Db 296 GATCTGGCAAAAGCAGGCTTTTACTACATAGGACTGGAGACAGAGTGCCTTGTGCTTGC 355
QY 121 TGTGTGGGAAAACTGAAAAATTTGGAACTTGTGATCGTGGCTGTGACAGACACAGGCGA 180
|||||
Db 356 TGTGTGGGAAAAATTTGAGCAATTTGGGACCGGAGGATAATGCTATGTCAGAACACCTGAGA 415

Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for high quality sequence is 20. Three-prime sequences, which are obtained with Polymix or T7 sequencing primer, are presented as the reverse complement.
Seq primer: JEN REV
High quality sequence stop: 534
POLYA-No.

FEATURES source
Location/Qualifiers
1..567
/organism="Equus caballus"
/db_xref="taxon:9796"
/clone_lib="Monocytes (MONO1)"
/cell_type="Isolated peripheral blood monocytes stimulated with E. coli lipopolysaccharide"
/note="Vector: pBluescript SK(-) from Lambda ZapII; Site.1: XhoI; Site.2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZapII. Clones to be sequenced were prepared by mass excision."
BASE COUNT 147 a 130 c 136 g 154 t
ORIGIN

Query Match 38.3%; Score 78.2; DB 13; Length 567;
Best Local Similarity 65.0%; Pred. No. 6.8e-16;
Matches 132; Conservative 0; Mismatches 68; Indels 3; Gaps 1;
QY 1 GAAGACCTAGATTAAAGTCTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60
DB 96 GAAAAGCCAGATATCTACTTCCAGATGTGGCC---GCTGACCTTCTGTGCCCAACA 152
QY 61 GAGTTAGCAAGTCTGGACCTTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTTGT 120
DB 153 GATCTGCAAAAGCTGGCTTTTACTACATAGAGCCGGGACAGAGTGGCTGCTTGGC 212
QY 121 TGTGGTGGAAACATGAAAATTTGGGAACCTTGTGATCGTCCCTGGTCAGAACACAGCGCA 180
DB 213 TGTGGTGGAAATTTGACAAATTTGGGAACCGAAGGATGATGCTATGTCGGAACACCTGAGA 272
QY 181 CACTTTCCTAATTCCTCTTTGT 203
DB 273 CATTTCCCAACTGCCCGTTGT 295

RESULT 13
LOCUS BI326908 512 bp mRNA linear EST 01-SEP-2001
DEFINITION AR071E101SPBE10S Infected Porcine Spleen cDNA library Sus scrofa cDNA, mRNA sequence.
ACCESSION BI326908
VERSION BI326908.1 GI:15416611
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 512)
AUTHORS Rink A., Santschi E.M. and Beattie C.W.
TITLE Amplified, Normalized cDNA Libraries from a Porcine Model of Orthopedic Implant Associated Staphylococcus aureus Infection
JOURNAL Unpublished (2001)
COMMENT Contact: Rink A
Department of Animal Biotechnology
College of Agriculture, Biotechnology and Natural Resources,
University of Nevada, Reno
MS 202, FA 103, 1664 N Virginia St, Reno, NV 89557-0236, USA
Tel: 775 784 1705
Fax: 775 784 1375
Email: arink@cabnr.unr.edu
Tissues and cells are derived from a porcine model for implant-associated infection using 1000 cfu of Staphylococcus aureus in a tibial transection, reduced and internally fixed with a dynamic compression plate. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The

adapter sequence is 'AATTCGGCAGGAG'.
Location/Qualifiers
1..512
/organism="Sus scrofa"
/strain="crossbreed"
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/clone_lib="Infected Porcine Spleen cDNA library"
/tissue_type="Spleen"
/cell_type="mixed"
/dev_stage="28 days post infection, 5 month old castrated male"
/lab_host="SOLR"
/note="Vector: pBSK; Site.1: Eco RI; Site.2: XhoI; Tissues and cells are derived from a porcine model for implant-associated infection using 1000 cfu of Staphylococcus aureus in a tibial transection, reduced and internally fixed with a dynamic compression plate. NOTE: The sequences contain a 'cDNA adapter' between the EcoRI site and the start of the EST. The adapter sequence is 'AATTCGGCAGGAG'.
BASE COUNT 136 a 108 c 113 g 145 t 10 others
ORIGIN

Query Match 37.5%; Score 76.6; DB 13; Length 512;
Best Local Similarity 64.5%; Pred. No. 2.3e-15;
Matches 131; Conservative 0; Mismatches 69; Indels 3; Gaps 1;
QY 1 GAAGACCTAGATTAAAGTCTTTCAGAACTGGCCAGACTATGCTCACCTAACCCCAAGA 60
DB 79 GAAAAGACAGATATCTACTTCCAGATGTGGCCA---TTGACCTTCTGTGCCCAACA 135
QY 61 GAGTTAGCAAGTCTGGACCTTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTTGT 120
DB 136 GATCTGCAAAAGCAGGCTTTTACTACATAGAGACCTGGACAGAGTGGCTTGTGCTGCC 195
QY 121 TGTGGTGGAAACATGAAAATTTGGGAACCTTGTGATCGTCCCTGGTCAGAACACAGCGCA 180
DB 196 TGTGGTGGAAATTTGACAAATTTGGGAACCGAAGGATGATGCTATGACAGAACACTTACGA 255
QY 181 CACTTTCCTAATTCCTCTTTGT 203
DB 256 CATTTCCCAACTGCCCATTTT 278

RESULT 14
LOCUS BM446366 459 bp mRNA linear EST 05-FEB-2002
DEFINITION IL16H6.ab1 Bos taurus ileum #1 library Bos taurus cDNA, mRNA sequence.
ACCESSION BM446366
VERSION BM446366.1 GI:18530522
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 459)
AUTHORS Hansen, C., Fu, A., Meng, Y., Li, C., Okine, E., Senses, C.W., Gordon, P.M.K. and Moore, S.S.
TITLE Gene Expression Profiling of the Bovine Gastrointestinal Tract Unpublished (2002)
COMMENT Contact: Dr. Stephen Moore
Beef Genomics Laboratory
Dept of AFNS, University of Alberta
410 Agri/For, Dept of AFNS, U of A, Edmonton, AB, T6G 2P5, Canada
Tel: 780 492 0169
Fax: 780 492 4265
Email: smoores@afns.ualberta.ca
Insert Length: 459 Std Error: 0.00
POLYA-No.
FEATURES source
Location/Qualifiers
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/cell_type="Simple columnar epithelial"
/dev_stage="Young adult"
/lab_host="X11-BlueMR/strain"
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EcoRI; Site_2: Xho I"
BASE COUNT      129 a 106 c 86 g 138 t
ORIGIN
Query Match
Best Local Similarity 37.1%; Score 75.6; DB 13; Length 459;
Matches 127; Conservative 0; Mismatches 64; Indels 3; Gaps 1;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCACCCTAACCCCAAGA 60
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Db 269 GAAAAAGCCAGATTACTTACCTTCCAGATGTGGCC---GTTGACTTTTCTGTCAACCAACA 325

QY 61 GAGTTAGCAAGTGCTGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTTGT 120
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 326 GACCTGGCAAAACAGCGCTTTTATTACATAGGACCTGGAGATAGAGTGGCTTGTGCTTGGC 385

QY 121 TGTGTGGAAACTGAAAAAATTGGGAACCTTGTGATCGTGGCTGCAGACACAGCGCA 180
|||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db 386 TGTGTGGAACTTGGCAATTGGGAACCGAAGGATGCTATGTCAGAACACCTGAGA 445

QY 181 CACTTTCCTAATTG 194
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Db 446 CATTTCCCAACTG 459

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RESULT 15
LOCUS   BM458775
DEFINITION
BM458775 959 bp mRNA linear EST 05-FEB-2002
AGENCOURT_6413630 NIH_MGC_85 Homo sapiens cDNA clone IMAGE:5497880
5', mRNA sequence.
ACCESSION
BM458775
VERSION
BM458775.1 GI:18507815
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 959)
NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS
National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE
Unpublished (1999)
JOURNAL
Contact: Robert Strausberg, Ph.D.
COMMENT
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Lou Staudt
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone Distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12128 row: 1 column: 09
High quality sequence stop: 729.
Location/Qualifiers
1..959
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/tissue_type="lymphoma, cell line"
/lab_host="DH10B (phage-resistant)"
/note="Organ: lymph; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.867 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."

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FEATURES
source

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BASE COUNT      288 a 215 c 174 g 281 t 1 others
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Query Match
Best Local Similarity 36.4%; Score 74.2; DB 13; Length 959;
Matches 136; Conservative 0; Mismatches 63; Indels 4; Gaps 2;

QY 1 GAAGAAGCTAGATTAAAGTCCTTTTCAGAACTGGCCAGACTATGCTCACCCTAACCCCAAGA 60
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QY 61 GAGTTAGCAAGTGCTGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTCTTTTGT 120
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QY 121 TGTGTGGAAACTGAAAAAATTGGGAACCTTGTGATCGTGGCTGCAGAACACAGCGCA 180
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Db 752 TGTGTGGAAATTTGAGCAATTGGGAACCC---GAAGATAATGCTATGTCAGAACACCTGAGA 810

QY 181 CACTTTCCTAATTGCTTCTTGT 203
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Db 811 CATTTCCCAAAATGCCCAATTAT 833

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Search completed: April 16, 2003, 00:54:54
Job time : 980.083 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:40:42 ; Search time 1001.52 Seconds
(without alignments)
5753.635 Million cell updates/sec

Title: US-09-654-743-47
Perfect score: 198
Sequence: 1 tatgaagcagcgtctttac.....atccagggtcgaatatctg 198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 3: gb_in.*
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- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	198	100.0	1659	6	E31042	E31042 Method for
2	198	100.0	1659	9	HSU32974	U32974 Human IAP-1
3	198	100.0	2086	9	BC032729	BC032729 Homo sapi
4	198	100.0	2404	6	AX429575	AX429575 Sequence
5	198	100.0	2540	6	AR103281	AR103281 Sequence
6	198	100.0	2540	6	AX412118	AX412118 Sequence
7	198	100.0	2540	9	HSU45880	U45880 Human X-lin
8	198	100.0	3000	6	AX412131	AX412131 Sequence
9	198	100.0	5232	6	AR106397	AR106397 Sequence
10	198	100.0	5232	6	AR116699	AR116699 Sequence
11	180.4	91.1	1752	6	AX104956	AX104956 Sequence
12	180.4	91.1	1752	9	AF164681	AF164681 Homo sapi
13	180.4	91.1	154214	9	AC079753	AC079753 Homo sapi
14	179.4	90.6	1491	10	AF183429	AF183429 Rattus no
15	179.4	90.6	2468	10	AB033366	AB033366 Rattus no
16	179.4	90.6	3032	10	AF304334	AF304334 Rattus no
17	177.8	89.8	2032	10	AF304333	AF304333 Rattus no
18	174.6	88.2	1988	10	MNU36842	U36842 Mus musculu
19	173	87.4	2100	6	AX412124	AX412124 Sequence
20	169.8	85.8	2691	6	AR106400	AR106400 Sequence
21	169.8	85.8	2691	6	AR116702	AR116702 Sequence
22	169.8	85.8	2691	10	MMU88990	U88990 Mus musculu
23	166	83.8	711	6	AX104970	AX104970 Sequence
24	166	83.8	711	9	AY030052	AY030052 Pan trogl
25	166	83.8	1758	6	AX370787	AX370787 Sequence
26	166	83.8	1758	6	AX370789	AX370789 Sequence
27	166	83.8	4993	6	AX104968	AX104968 Sequence
28	166	83.8	4993	9	AF164682	AF164682 Homo sapi
29	166	83.8	144301	9	AC010467	AC010467 Homo sapi
30	166	83.8	165662	9	AC092070	AC092070 Homo sapi
31	164.4	83.0	711	6	AR121220	AR121220 Sequence
32	164.4	83.0	711	6	AR123871	AR123871 Sequence
33	164.4	83.0	2032	9	AF420440	AF420440 Homo sapi
34	162.8	82.2	711	6	AX104972	AX104972 Sequence
35	162.8	82.2	711	9	AY030053	AY030053 Gorilla g
36	146.6	74.0	187568	9	AP002967	AP002967 Homo sapi
37	145	73.2	184439	2	AP003085	AP003085 Homo sapi
38	132.6	67.0	327	4	AF458770	AF458770 Bos tauru
39	105	53.0	133391	9	HSJ31561	HSJ31561 Human DNA
40	105	53.0	201197	2	HS242412	HS242412 Homo sapien
41	100.4	50.7	1740	5	AF451854	AF451854 Gallus ga
42	96.8	48.9	158093	9	AL390123	AL390123 Human DNA
43	79.2	40.0	1770	10	AF183431	AF183431 Rattus no
44	78.6	39.7	2563	9	HUMSCP8	L9432 Homo sapien
45	78.6	39.7	2601	6	ARI29833	ARI29833 Sequence

ALIGNMENTS

RESULT 1
E31042
LOCUS E31042 1659 bp DNA linear PAT 18-JUN-2001
DEFINITION Method for screening substance inhibiting binding to XIAP.
ACCESSION E31042
VERSION E31042.1 GI:13017307
KEYWORDS JP 1999326328-A/2.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1659)
AUTHORS Kunihiro,M.
TITLE Method for screening substance inhibiting binding to XIAP
JOURNAL Patent: JP 1999326328-A 2 26-NOV-1999;
KUNIHIRO MATSUMOTO

Tissue Procurement: ATCC
 cDNA Library Preparation: Life Technologies, Inc.
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mc@nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Breen, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granice, S., Guan, X., Gupta, J., Haghghi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Tsurgeon, C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 69 Row: 1 Column: 18
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4502142.

FEATURES

source

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CDS

BASE COUNT

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QY 1 TATGAACGACGGATCTTTACTTTTGGGACATGGATATACAGTAAACAGGACGAGCTT 60
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 Db 931 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 990
 QY 121 GGAGGGCTAACTGATTTGAAGCCAGTGAGACCCCTTTGGGAAACAACATGCTAAATGGTAT 180
 Db 991 GGAGGGCTAACTGATTTGAAGCCAGTGAGACCCCTTTGGGAAACAACATGCTAAATGGTAT 1050
 QY 181 CCAGGGTGCAAAATATCTG 198
 Db 1051 CCAGGGTGCAAAATATCTG 1068
 RESULT 4
 AX429575
 LOCUS 2404 bp DNA linear PAT 21-JUN-2002

DEFINITION Sequence 38 from Patent WO0226820.

ACCESSION AX429575

VERSION AX429575.1 GI:21540833

KEYWORDS human.

ORGANISM Homo sapiens

REFERENCE 1
 AUTHORS Cohen, D., Dengler, U.J., Finelli, A.L., Freuler, F., Konsolaki, M.,
 Reinhardt, M.W. and Zisman, S.
 TITLE Transgenic drosophila melanogaster expressing beta amyloid
 JOURNAL Patent: WO 0226820-A 38 04-APR-2002;
 NOVARTIS ERFINO VERWALT GMBH (AT)

FEATURES

source

1. .2404

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/db_xref="taxon:9606"

BASE COUNT 759 a 372 c 525 g 748 t

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 QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120
 Db 887 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 946
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 QY 181 CCAGGGTGCAAAATATCTG 198
 Db 1007 CCAGGGTGCAAAATATCTG 1024
 RESULT 5
 AR103281
 LOCUS Sequence 1 from patent US 6087173.
 DEFINITION Sequence 1 from patent US 6087173.
 ACCESSION AR103281
 VERSION AR103281.1 GI:12814869
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 2540)
 AUTHORS Bennett, C. Frank, Ackermann, E. J. and Cowser, L. M.
 TITLE Antisense modulation of X-linked inhibitor of apoptosis expression
 JOURNAL Patent: US 6087173-A 1 11-JUL-2000;
 FEATURES Location/Qualifiers
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 /organism="unknown"

BASE COUNT 781 a 415 c 571 g 773 t

ORIGIN

Query Match 100.0%; Score 198; DB 6; Length 2540;
 Best Local Similarity 100.0%; Pred. No. 2.3e-44;
 Matches 198; Conservative 0; Mismatches 0; Indels 1; Gaps 0;

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 QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120
 Db 886 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 945

QY 121 GGAGGGCTAACTGATGGAGCCAGTGAAGACCCCTGGGAACAACATGCTAAATGGTAT 180
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Db 946 GGAGGGCTAACTGATGGAGCCAGTGAAGACCCCTGGGAACAACATGCTAAATGGTAT 1005
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QY 181 CCAGGGTGCAATATCTG 198
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Db 1006 CCAGGGTGCAATATCTG 1023
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RESULT 6
AX412118 2540 bp DNA linear PAT 14-JUN-2002
LOCUS
DEFINITION Sequence 218 from Patent WO0226968.
ACCESSION AX412118
VERSION
AX412118.1 GI:21444581
KEYWORDS
SOURCE human..

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.
Antisense iap nucleic acids and uses thereof
Patent: WO 0226968-A 218 04-APR-2002;
University of Ottawa (CA); Aegera Therapeutics Inc. (CA)

FEATURES
Location/Qualifiers
1..2540
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BASE COUNT 781 a 415 c 570 g 773 t 1 others
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Query Match 100.0%; Score 198; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 120
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QY 181 CCAGGGTGCAATATCTG 198
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Db 1006 CCAGGGTGCAATATCTG 1023
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RESULT 7
HSU45880 2540 bp mRNA linear PRI 16-FEB-1996
LOCUS
DEFINITION Human X-linked inhibitor of apoptosis protein XIAP mRNA, complete
cds.
U45880
VERSION
U45880.1 GI:1184319
KEYWORDS
SOURCE Homo sapiens.

ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
1 (bases 1 to 2540)
Liston, P., Roy, N., Tamai, K., Lefebvre, C., Baird, S.,
Cherton-Horvat, G., Farahani, R., McLean, M., Ikeda, J., MacKenzie, A.
and Korneluk, R.G.
Suppression of apoptosis in mammalian cells by XIAP and a related
family of IAP genes
Nature 379 (6563), 349-353 (1996)

MEDLINE 96149249
PUBMED 8552191
REFERENCE 2 (bases 1 to 2540)
AUTHORS Baird, S.D.
TITLE Direct Submission
JOURNAL Submitted (16-JAN-1996) Stephen D. Baird, Children's Hospital of
Eastern Ontario, Genetics, 401 Smyth Rd., Ottawa, Ontario, K1H 8L1,
Canada

FEATURES
Location/Qualifiers
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/map="Xq24-25"
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34..1527
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TOSTNSGIONQYKVENYLGSRDHFALDRPSETHADYLLRTGVGVDSIDTIYPRNPAM
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EHRHFPNCFVVLGRNLNRSSEDAVSSDRNPNSNLPNPSMADYEAFITFTGTWI
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MEEKIQISGNSYKSLVLAIVADLVNAQKSDQSSQTSLOKEISTEIRQLRLOEERLC
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826..1020
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1381..1485
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BASE COUNT 781 a 415 c 571 g 773 t
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2.3e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGACATGGATATACCTACAGTTACACAGGAGCAGCTT 60
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Db 826 TATGAAGCAGCGATCTTTACTTTTGGACATGGATATACCTACAGTTACACAGGAGCAGCTT 885
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QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 120
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Db 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTCACTGTGGA 945
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QY 121 GGAGGGCTAACTGATGGAGCCAGTGAAGACCCCTGGGAACAACATGCTAAATGGTAT 180
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Db 946 GGAGGGCTAACTGATGGAGCCAGTGAAGACCCCTGGGAACAACATGCTAAATGGTAT 1005
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QY 181 CCAGGGTGCAATATCTG 198
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Db 1006 CCAGGGTGCAATATCTG 1023
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RESULT 8
AX412131 3000 bp DNA linear PAT 14-JUN-2002
LOCUS
DEFINITION Sequence 231 from Patent WO0226968.
ACCESSION AX412131
VERSION
AX412131.1 GI:21444588
KEYWORDS
SOURCE human..

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.
TITLE Antisense iap nucleic acids and uses thereof
JOURNAL Patent: WO 0226968-A 231 04-APR-2002;
University of Ottawa (CA); Aegera Therapeutics Inc. (CA)
FEATURES
source Location/Qualifiers
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/db_xref="taxon:9606"
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Db 1542 GCAAGAGCTGGATTTATGCTTTTAGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGA 1601
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Db 1602 GGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 1661
Qy 181 CCAGGTCGAATATCTG 198
Db 1662 CCAGGTCGAATATCTG 1679
RESULT 9
AR106397
LOCUS AR106397 5232 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 3 from patent US 6107041.
ACCESSION AR106397
VERSION AR106397.1 GI:12820927
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5232)
AUTHORS Korneluk, R.G., MacKenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.
TITLE Detection and modulation of IAPs for the diagnosis and treatment of
JOURNAL proliferative disease
PATENT: US 6107041-A 3 22-AUG-2000;
LOCATION/Qualifiers
FEATURES
source 1..5232
/organism="unknown"
BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 TATGAAGCAGGATCTTTACTTTTGGGACATGGATATCTACTCAGTTAACAGGAGCAGCTT 60
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Qy 61 GCAAGAGCTGGATTTATGCTTTTAGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTTATGCTTTTAGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGA 945
Qy 121 GGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 180
Db 946 GGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 1005
RESULT 11
AR104956
LOCUS AR104956 1752 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 1 from Patent WO0123368.
ACCESSION AR104956
VERSION AR104956.1 GI:13921153
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1752)
REFERENCE
AUTHORS Duckett, C. and Mir, S.S.
TITLE Members of the iap gene family
JOURNAL Patent: WO 0123568-A 1 05-APR-2001;
THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
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847..1197
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CDS

Qy 181 CCAGGTCGAATATCTG 198
Db 1006 CCAGGTCGAATATCTG 1023
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LOCUS AR116699 5232 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 3 from patent US 6133437.
ACCESSION AR116699
VERSION AR116699.1 GI:14097021
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 5232)
AUTHORS Korneluk, R.G., MacKenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.
TITLE Modulation of IAPs for the treatment of proliferative diseases
JOURNAL Patent: US 6133437-A 3 17-OCT-2000;
LOCATION/Qualifiers
FEATURES
source 1..5232
/organism="unknown"
BASE COUNT 1579 a 861 c 1062 g 1728 t 2 others
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Query Match 100.0%; Score 198; DB 6; Length 5232;
Best Local Similarity 100.0%; Pred. No. 2.1e-44;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy 121 GGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 180
Db 946 GGAGGCTTAAGTGAAGCCAGTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 1005
RESULT 11
AR104956
LOCUS AR104956 1752 bp DNA linear PAT 30-APR-2001
DEFINITION Sequence 1 from Patent WO0123368.
ACCESSION AR104956
VERSION AR104956.1 GI:13921153
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1752)
REFERENCE
AUTHORS Duckett, C. and Mir, S.S.
TITLE Members of the iap gene family
JOURNAL Patent: WO 0123568-A 1 05-APR-2001;
THE DEPARTMENT OF HEALTH AND HUMAN SERVICES (US)
FEATURES
source Location/Qualifiers
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BASE COUNT 530 a 299 c 385 g 538 t
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Best Local Similarity 94.4%; Pred. No. 1.7e-39;
Matches 187; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

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DB 499 TATGAAGCATGGATCATTTACCTTTTGGGATGGATATATTCAGTTAAACAAGGACGCTT 558
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DB 619 GGGGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACACATGATAAATGGCAT 678
QY 181 CCAGGGTCAAAATATCTG 198
DB 679 CCAGGGTCAAAATATCTG 696

RESULT 12
AF164681 AF164681 1752 bp DNA linear PRI 31-JUL-2001
LOCUS
DEFINITION Homo sapiens IAP-like protein 3 (ILP3) gene, complete cds.
ACCESSION AF164681
VERSION AF164681.1 GI:15042061
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1752)
AUTHORS Mir, S.S. and Duckett, C.S.
TITLE Molecular cloning of human homologs of IAP-like protein
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 1752)
AUTHORS Mir, S.S. and Duckett, C.S.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-1999) Metabolism Branch, National Cancer
Institute, 10 Center Drive, Room 6B-05, Bethesda, MD 20892-1578,
USA

FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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BASE COUNT 530 a 299 c 385 g 538 t
ORIGIN

Query Match 91.1%; Score 180.4; DB 9; Length 1752;

Best Local Similarity 94.4%; Pred. No. 1.7e-39;
Matches 187; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACCTTTTGGGACATGGATATACCTAGTTAAACAAGGACGCTT 60
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QY 61 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACTGTGGA 120
DB 559 TCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACTGTGGA 618
QY 121 GGAGGGCTAACTGATTTGAAGCCAGTGAAGACCCCTTGGGAACACATGCTAAATGGTAT 180
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DB 679 CCAGGGTCAAAATATCTG 696

RESULT 13
AC079753 AC079753 154214 bp DNA linear PRI 01-MAR-2002
LOCUS
DEFINITION Homo sapiens BAC clone RP11-67L14 from 2, complete sequence.
ACCESSION AC079753
VERSION AC079753.7 GI:14318395
KEYWORDS HTG.
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 154214)
AUTHORS Sulston, J.E. and Waterston, R.
TITLE Toward a complete human genome sequence
JOURNAL Genome Res. 8 (11), 1097-1108 (1998)
MEDLINE 99063792
PUBMED 9847074

REFERENCE 2 (bases 1 to 154214)
AUTHORS Andrews, S., Cotton, M., Doebber, A. and Rose, C.
TITLE The sequence of Homo sapiens BAC clone RP11-67L14
JOURNAL Unpublished (2001)
REFERENCE 3 (bases 1 to 154214)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

REFERENCE 4 (bases 1 to 154214)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (06-JUN-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
REFERENCE 5 (bases 1 to 154214)
AUTHORS Waterston, R.H.
TITLE Direct Submission
JOURNAL Submitted (03-JUL-2001) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA

REFERENCE 6 (bases 1 to 154214)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (09-JAN-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
REFERENCE 7 (bases 1 to 154214)
AUTHORS Waterston, R.
TITLE Direct Submission
JOURNAL Submitted (01-MAR-2002) Department of Genetics, Washington
University, 4444 Forest Park Avenue, St. Louis, Missouri 63108, USA
On Jun 6, 2001 this sequence version replaced gi:14029079.

Center: Washington University Genome Sequencing Center
Center code: WUGSC

Web site: <http://genome.wustl.edu/gsc>
 Contact: sapiens@genome.wustl.edu
 ----- Summary Statistics -----
 Center project name: H_NH0067L14

NOTICE: This sequence may not represent the entire insert of this clone. It may be shorter because we only sequence overlapping clone sections once, or longer because we provide a small overlap between neighboring data submissions.

This sequence was finished as follows unless otherwise noted: all regions were double stranded, sequenced with an alternate chemistry, or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by sequence from more than one subclone; and the assembly was confirmed by restriction digest.

MAPPING INFORMATION:

Mapping information for this clone was provided by Dr. John D. McPherson, Department of Genetics, Washington University, St. Louis MO. For additional information about the map position of this sequence, see <http://genome.wustl.edu/gsc>

SOURCE INFORMATION:

The RPII-11 human BAC library was made from the blood of one male donor, as described by Osoegawa, K., Woon, P.Y., Zhao, B., Frengen, E., Tatenno, M., Catanese, J.J. and de Jong, P.J. (1998) An improved approach for construction of bacterial artificial chromosome libraries. Genomics 51:1-8. The clone may be obtained either from Research Genetics, Inc. (<http://www.resgen.com>) or Pieter de Jong and coworkers at <http://www.chori.org>
 VECTOR: pBAC3.6

NEIGHBORING SEQUENCE INFORMATION:

The clone sequenced to the right is RP11-725J3. Actual start of this clone is at base position 1 of RP11-67L14; actual end is at base position 154214 of RP11-67L14.

There are polymorphic base differences in the overlap between

RP11-67L14 and RP11-725J3.

FEATURES

Source

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 /db_xref="taxon:9606"
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repeat_region	2409. .2607	/rpt_family="MIR"
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misc_feature	2589. .3114	/note="match to EST AW173248 (NID:g6439196) xj85b09.x1"
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repeat_region	3777. .4070	/rpt_family="Alu"
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repeat_region	4909. .5315	/rpt_family="MaLR"
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repeat_region	6351. .7343	/rpt_family="(T)n"
repeat_region	7333. .7357	/rpt_family="MaLR"
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repeat_region	9340. .9479	/rpt_family="MaLR"
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repeat_region	12933. .13311	/rpt_family="MaLR"
repeat_region	13197. .13202	/rpt_family="L2"
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repeat_region	14162. .14339	/rpt_family="Alu"
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repeat_region	14451. .14580	/rpt_family="L2"
repeat_region	15272. .15565	/rpt_family="Alu"
repeat_region	15618. .15703	/rpt_family="L1"
repeat_region	15922. .15942	/rpt_family="CT-rich"
repeat_region	15944. .16120	/rpt_family="(TTTC)n"
repeat_region	16110. .16409	/rpt_family="Alu"
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repeat_region	16954. .17243	/rpt_family="CR1"
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repeat_region	17566. .17715	/rpt_family="MER2_type"
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QY 181 CCAGGGTGCATAATATCT 197
Db 1299 CCAGGGTGTAAATATCT 1315

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Job time : 1023.52 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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3369.223 Million cell updates/sec

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Perfect score: 198
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SID52/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	1659	AAZ48862	Human XIAP coding
2	198	100.0	2404	AAK99405	DNA of APP related
3	198	100.0	2540	AAT70836	Human apoptosis in
4	198	100.0	2540	AAA64901	Human X-linked inh
5	198	100.0	2540	ABK93869	Human CDNA encodin
6	198	100.0	3000	ABK93875	Human CDNA encodin
7	198	100.0	5232	AAV55038	Human XIAP coding
8	180.4	91.1	1752	AAAD03575	Human IAP-like pro
9	174.6	88.2	1988	AAT72710	Mouse inhibitor of

10	173	87.4	2100	18	AAT70839	Mouse apoptosis in
11	173	87.4	2100	24	ABK93872	Mouse cDNA encodin
12	169.8	85.8	2691	19	AAV55041	Murine XIAP coding
13	166	83.8	711	22	AAV55041	Chimpanzee IAP-like
14	166	83.8	1758	24	ABK14677	Human inhibitor of
15	166	83.8	1758	24	ABK14678	Human inhibitor of
16	166	83.8	4993	22	AAAD03581	Human IAP-like pro
17	164.4	83.0	711	21	AAA06940	DNA encoding human
18	164.4	83.0	1559	24	ABK13197	Human testes speci
19	162.8	82.2	711	22	AAAD03583	Gorilla IAP-like p
20	157.8	79.7	578	22	AAAD02960	Human IL-1ra BAC c
21	131.4	66.4	802	20	AAAD03018	Human IL-1ra BAC c
22	96.8	48.9	302	24	ABK93875	Human colon cancer
23	83	41.9	1402	20	AAK93875	Human IL-1ra BAC c
24	78.6	39.7	2601	18	AAT61591	Human c-IAP2, Hom
25	78.6	39.7	2666	18	AAT70837	Human apoptosis in
26	78.6	39.7	2676	24	ABK93870	Human CDNA encodin
27	78.6	39.7	3076	18	AAT72712	Human inhibitor of
28	78.6	39.7	3076	20	AAZ41005	Human inhibitor inh
29	78.6	39.7	3076	20	AAZ22096	Human cellular inh
30	78.6	39.7	3076	24	ABL62746	Breast cancer rela
31	78.6	39.7	3076	24	ABL66325	Lung cancer relate
32	78.6	39.7	3734	22	AAK90972	Human API2-MIT chi
33	78.6	39.7	3734	24	ABK52387	DNA encoding cysti
34	78.6	39.7	6669	19	AAV55039	Human HIAP-1 codin
35	78.6	39.7	6669	24	ABK93876	Human CDNA encodin
36	74.4	37.6	1435	17	AAT43709	Human inhibitor of
37	74.4	37.6	2580	18	AAT70838	Human apoptosis in
38	74.4	37.6	2580	24	ABK93871	Human CDNA encodin
39	74.4	37.6	2589	18	AAT61590	Human c-IAP1, Hom
40	74.4	37.6	3532	18	AAT72711	Human inhibitor of
41	74.4	37.6	3532	20	AAZ22143	Human cellular inh
42	74.4	37.6	3532	24	ABN96857	Gene #3355 used to
43	74.4	37.6	3732	19	AAV55040	Human HIAP-2 codin
44	71.2	36.0	2862	18	AAT61592	Murine c-IAP, Mus
45	71.2	36.0	3151	19	AAV55043	Murine HIAP-2 codi

ALIGNMENTS

RESULT 1
AAZ48862
ID AAZ48862 standard; CDNA; 1659 BP.

AC AAZ48862;

XX 24-MAR-2000 (first entry)

DT Human XIAP coding sequence.

DE

XX Human: TAB1; XIAP; X-linked inhibitor of apoptosis

KW transforming growth factor-beta activated kinase 1

KW TAK1 binding protein 1; extracellular matrix protein production;

KW cell growth inhibitor; beta-amyloid protein deposition;

KW immunosuppression; Transforming growth factor-beta

OS Homo sapiens.

XX JP11326328-A.

XX 26-NOV-1999.

XX 13-MAY-1998; 98JP-0130378.

XX 13-MAY-1998; 98JP-0130378.

XX (MATS/) MATSUMOTO K.

XX WPI: 2000-078337/07.

XX P-PSDB; AAY59451.

PT Screening a substance which inhibits combination of the X-linked

PT inhibitor of apoptosis protein

PS Disclosure; Page 28-30; 43pp; Japanese.

XX This sequence encodes the human XIAP protein.

CC The invention relates to a method for screening a substance inhibiting
CC the formation of a complex between XIAP and TAB1, in which X-linked
CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta
CC activated kinase 1 (TAK1) binding protein (TAB1) and a substance to be
CC tested are contacted with each other and then the presence or formation
CC of a complex between XIAP and TAB1 is detected. The substance can be used
CC as a drug for extracellular matrix protein production enhancement, cell
CC growth inhibition, monocyte migration, physiologically active substance
CC induction, immunosuppression, and beta-amyloid protein deposition. A
CC substance inhibiting the formation of a complex between TAB1 and XIAP as
CC well as between XIAP and TGF-beta (Transforming growth factor-beta) type
CC I and/or type II receptor is useful as a drug.

XX Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;

Query Match 100.0%; Score 198; DB 21; Length 1659;

Best Local Similarity 100.0%; Pred. No. 1.7e-54;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCTTTACTTTTGGGACATGGATATCTACTCAGTTAAAGGACGAGCTT 60

DB 874 TATGAGCAGCGATCTTTACTTTTGGGACATGGATATCTACTCAGTTAAAGGACGAGCTT 933

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACCTGTGGA 120

DB 934 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGATAAAGTCTTTCACCTGTGGA 993

QY 121 GGAGGGCTAACTGATTTGGAAGCCAGTGAAGCCCTTGGGAAACACATGCTAAATGGTAT 180

DB 994 GGAGGGCTAACTGATTTGGAAGCCAGTGAAGCCCTTGGGAAACACATGCTAAATGGTAT 1053

QY 181 CCAGGGTGCAAAATATCTG 198

DB 1054 CCAGGGTGCAAAATATCTG 1071

RESULT 2

AAK99405

ID AAK99405 standard; DNA; 2404 BP.

XX AC AAK99405;

XX 27-JUN-2002 (first entry)

XX DNA of APP related human homologue hcp35211.

XX Neuroprotective; nontropic; transgenic fly; Alzheimer's disease; Abeta;

XX amyloid precursor protein; tissue-specific expression control; human APP;

XX APP pathway modulator; gene therapy; gene; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 692..1528

XX /*tag= a

XX /product= "Protein of human homologue hcp35211"

XX /note= "No start codon"

XX WO200226820-A2.

XX 04-APR-2002.

XX 01-OCT-2001; 2001WO-EP11345.

XX 29-SEP-2000; 2000US-236893P.

XX 14-JUN-2001; 2001US-298309P.

XX (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH:

XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;

PI Reinhardt MWM, Zusman S;

XX WPI: 2002-315796/35.

DR P-PSDB; AAO20511.

XX New transgenic fly, containing DNA encoding an Abeta portion of human

PT APP, useful for identifying agents which modulate the APP pathway and

PT which can be used to treat Alzheimer's disease

XX Example 4; Page 111; 129pp; English.

XX The invention relates to a transgenic fly whose genome comprises DNA

CC encoding a polypeptide having the Abeta portion of human amyloid

CC precursor protein (APP), fused to a signal sequence. The DNA sequence

CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in

CC the specification. The DNA sequence is operably linked to a tissue-

CC specific expression control sequence. Expression of the sequence gives

CC the fly an altered phenotype. The purpose of the invention is for

CC identifying agents that inhibit or promote the expression and/or function

CC of genes or encoded polypeptides which modify the APP pathway. The agent

CC is a compound, triple helix DNA, antisense oligonucleotide, double

CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used

CC to treat conditions such as Alzheimer's disease. The agent can be used as

CC an APP pathway modulator or in gene therapy. This polynucleotide sequence

CC represents the DNA of the APP related human homologue hcp35211.

XX Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 other;

Query Match 100.0%; Score 198; DB 24; Length 2404;

Best Local Similarity 100.0%; Pred. No. 1.9e-54;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAGCAGCGATCTTTACTTTTGGGACATGGATATCTACTCAGTTAAAGGACGAGCTT 60

DB 827 TATGAGCAGCGATCTTTACTTTTGGGACATGGATATCTACTCAGTTAAAGGACGAGCTT 886

QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACCTGTGGA 120

DB 887 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGTGATAAAGTAAAGTCTTTCACCTGTGGA 946

QY 121 GGAGGGCTAACTGATTTGGAAGCCAGTGAAGCCCTTGGGAAACACATGCTAAATGGTAT 180

DB 947 GGAGGGCTAACTGATTTGGAAGCCAGTGAAGCCCTTGGGAAACACATGCTAAATGGTAT 1006

QY 181 CCAGGGTGCAAAATATCTG 198

DB 1007 CCAGGGTGCAAAATATCTG 1024

RESULT 3

AAK70836

ID AAT70836 standard; cDNA; 2540 BP.

XX AC AAT70836;

XX 02-SEP-1997 (first entry)

XX Human apoptosis inhibitor xiap cDNA.

XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;

XX XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;

XX ischaemia; myocardial infarction; stroke;

XX reperfusion injury; toxin-induced liver disease; gene therapy;

XX diagnosis; ds.

XX Homo sapiens.

XX Key Location/Qualifiers

XX CDS 34..1527

XX /*tag= a


```

XX PN WO9706255-A2.
XX PD 20-FEB-1997.
XX PF 05-AUG-1996; 96WO-IB01022.
XX PR 22-DEC-1995; 95US-0576956.
XX PR 04-AUG-1995; 95US-0511485.
XX PA (UYOT-) UNIV OTTAWA.
XX PI Baird S Korneluk RG, Liston P, Mackenzie AE;
XX DR WPI; 1997-154262/14.
XX DR P-PSDB; AAW19581.
XX PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
XX PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
XX PT of susceptibility to apoptotic disease
XX PS Claim 12; Page 67-68; 219pp; English.
XX CC Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and
XX CC hiap-2 genes (AA70836-41) respectively code for a new class of
XX CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis
XX CC (IAP). The xiap gene (for X-linked IAP gene) was isolated from a
XX CC human foetal brain ZapII cDNA library using an X-linked sequence
XX CC tag site that shows strong homology with the conserved ring zinc
XX CC finger domain of baculovirus CpiAP and OpiAP genes. The gene was
XX CC assigned to chromosome Xq25 by FISH. IAP nucleic acids can be used
XX CC to express IAP polypeptides in cells and animals to inhibit
XX CC apoptosis, and as primers and probes to identify and isolate
XX CC additional IAP genes, as well as in methods for treating diseases
XX CC and disorders involving apoptosis (anti-apoptotic gene therapy).
XX SQ Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 1 other;

Query Match 100.0%; Score 198; DB 18; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATACTCAGTTAAAGGAGCAGCTT 60
DB 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATACTCAGTTAAAGGAGCAGCTT 85
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCTTCACTGTGGA 120
DB 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCTTCACTGTGGA 120
QY 121 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGAAACACATGCTAAATGGTAT 180
DB 121 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGAAACACATGCTAAATGGTAT 180
QY 181 CCAGGGTGCAAAATATCTG 198
DB 181 CCAGGGTGCAAAATATCTG 198
QY 1006 CCAGGGTGCAAAATATCTG 1023
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 4
AAA64901
ID AAA64901 standard; DNA; 2540 BP.
XX AAA64901;
XX 07-NOV-2000 (first entry)
XX Human X-linked inhibitor of apoptosis DNA.
XX X-linked inhibitor of apoptosis; XIAP; hIAP; MIHA; U45880;
XX antisense; antiinflammatory; cytostatic; tumour; ds.
XX Homo sapiens.

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XX PH Key Location/Qualifiers
XX FT 34..1527
XX FT /*tag= a.
XX FT /product= "X-linked inhibitor of apoptosis"
XX PN US6087173-A.
XX PD 11-JUL-2000.
XX PF 09-SEP-1999; 99US-0392580.
XX PR 09-SEP-1999; 99US-0392580.
XX PA (ISIS-) ISIS PHARM INC.
XX PI Bennett CF, Cowser LM, Ackermann EJ;
XX DR WPI; 2000-498201/44.
XX DR P-PSDB; AAY9985.
XX PT Antisense compound useful for research reagents, diagnostics,
XX PT prophylaxis and for treating disorders associated with X-linked
XX PT inhibitor of apoptosis, modulates expression of X-linked inhibitor of
XX PS apoptosis
XX PS Example 13; Column 43-48; 33pp; English.
XX CC The present invention relates to antisense oligonucleotides designed to
XX CC inhibit expression of the human X-linked inhibitor of apoptosis. The
XX CC present sequence is the X-linked inhibitor of apoptosis DNA.
XX CC Modified phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are
XX CC more effective inhibitors than unmodified oligonucleotides. The
XX CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
XX CC expression in cells and tissues in vitro. The oligonucleotides are also
XX CC useful for treating animals or humans, prone to a disease associated
XX CC with X-linked inhibitor of apoptosis. The oligonucleotides may also be
XX CC used prophylactically to prevent infection, inflammation or tumour
XX CC formation.
XX SQ Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 other;

Query Match 100.0%; Score 198; DB 21; Length 2540;
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATACTCAGTTAAAGGAGCAGCTT 60
DB 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATACTCAGTTAAAGGAGCAGCTT 85
QY 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCTTCACTGTGGA 120
DB 61 GCAAGAGCTGGATTTTATGCTTTTAGGTGAAGGTGATAAAGTAAAGTGCTTCACTGTGGA 120
QY 121 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGAAACACATGCTAAATGGTAT 180
DB 121 GGAGGGCTAACTGATTGGAGCCAGTGAAGACCCCTTGGGAAACACATGCTAAATGGTAT 180
QY 181 CCAGGGTGCAAAATATCTG 198
DB 181 CCAGGGTGCAAAATATCTG 198
QY 1006 CCAGGGTGCAAAATATCTG 1023
DB 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 5
ABK93869
ID ABK93869 standard; cDNA; 2540 BP.
XX ABK93869;
XX 26-AUG-2002 (first entry)
XX Human cDNA encoding inhibitor of apoptosis, XIAP #1.

```

KW Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200226968-A2.
 XX
 XX 04-APR-2002.
 PD
 XX 27-SEP-2001; 2001WO-CA01379.
 PF
 XX 28-SEP-2000; 2000US-0672717.
 PR
 XX (UYOT-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX
 DR WPI: 2002-479562/51.
 DR P-PSDB: ABG65663.
 DR
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for
 PT enhancing apoptosis in a cell, for treating cancer and other
 PT proliferative diseases -
 XX
 XX Disclosure; Fig 1; 135pp; English.
 PS
 XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (1) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC cDNA sequence.
 XX
 SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;
 Query Match 100.0%; Score 198; DB 24; Length 2540;
 Best Local Similarity 100.0%; Pred. No. 1.9e-54;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 TATGAACGCGGATCTTTACTTTTGGGACATGGATATCTACTCAGTTACAGGACGCTT 60
 DB 826 TATGAACGCGGATCTTTACTTTTGGGACATGGATATCTACTCAGTTACAGGACGCTT 885
 QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATTAAGTCTTTCTACTGTGGA 120
 DB 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATTAAGTCTTTCTACTGTGGA 945
 QY 121 GGAGGGCTAACTGATTTGAAGCCAGTGAAGCCCTTTGGGAACAACATGCTAAATGCTAT 180
 DB 946 GGAGGGCTAACTGATTTGAAGCCAGTGAAGCCCTTTGGGAACAACATGCTAAATGCTAT 1005
 QY 181 CCAGGGTCCAAATATCTG 198
 DB 1006 CCAGGGTCCAAATATCTG 1023

RESULT 6

ABK93875
 ID ABK93875 standard; cDNA; 3000 BP.
 XX
 AC ABK93875;
 XX

DT 26-AUG-2002 (first entry)
 XX

XX Human cDNA encoding inhibitor of apoptosis, XIAP #2.
 DE

KW Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200226968-A2.
 XX
 XX 04-APR-2002.
 PD
 XX 27-SEP-2001; 2001WO-CA01379.
 PF
 XX 28-SEP-2000; 2000US-0672717.
 PR
 XX (UYOT-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX
 DR WPI: 2002-479562/51.
 DR
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for
 PT enhancing apoptosis in a cell, for treating cancer and other
 PT proliferative diseases -
 XX

Example 2; Fig 15; 135pp; English.
 PS

XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (1) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC cDNA sequence.
 XX

SQ Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 other;
 Query Match 100.0%; Score 198; DB 24; Length 3000;
 Best Local Similarity 100.0%; Pred. No. 2e-54;
 Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAACGCGGATCTTTACTTTTGGGACATGGATATCTACTCAGTTACAGGACGCTT 60
 DB 1482 TATGAACGCGGATCTTTACTTTTGGGACATGGATATCTACTCAGTTACAGGACGCTT 1541

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATTAAGTCTTTCTACTGTGGA 120
 DB 1542 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATTAAGTCTTTCTACTGTGGA 1601

QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGACACATGCTAAATGGTAT 180
Db 1602 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGACACATGCTAAATGGTAT 1661
QY 181 CCAGGGTGCAAAATATCTG 198
Db 1662 CCAGGGTGCAAAATATCTG 1679

RESULT 7
AAV55038
ID AAV55038 standard; cDNA; 5232 BP.
XX
AC AAV55038;
XX
DT 13-NOV-1998 (first entry)
XX
DE Human XIAP coding sequence.
XX
KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 34..1527
FT /*tag= a
FT /product= XIAP
XX
XX WO9835693-A2.
XX 20-AUG-1998.
XX 13-FEB-1998; 98WO-IB00781.
XX 13-FEB-1997; 97US-0800929.
XX (UYOT-) UNIV OTTAWA.
XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
XX Tsang B;
XX WPI: 1998-467164/40.
XX P-PSDB: AAW69294.

Inducing apoptosis in proliferative mammalian cells with inhibitor of IAP or NAIP polypeptide - also methods for prognosis based on presence of IAP and NAIP, specifically applied to cancers involving p53 mutations
XX
XX Claim 13; Fig 1; 147pp; English.

This sequence encodes the human XIAP protein, which is an inhibitor of apoptosis protein (IAP), and can be used in the method of the invention. The method is for enhancing apoptosis in cells from a mammal with proliferative disease by treatment with a compound that inhibits biological activity of an IAP or NAIP polypeptide. The inhibitory compounds are used to treat proliferative diseases, specially cancers of ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney, liver nasopharynx, thyroid, central nervous system, prostate, colon, rectum, cervix or endometrium, particularly to increase their sensitivity to chemotherapeutic agents. High levels of the IAP or NAIP proteins are detected in many cancers and are associated with poor prognosis, resistance to chemotherapeutic agents and mutations in p53 (it is suggested that wild-type p53 suppresses transcription of the IAP or NAIP genes). Transgenic animals are used for testing the effects of antisense oligonucleotides and for screening for the inhibitors.

Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;
Query Match 100.0%; Score 198; DB 19; Length 5232;
Best Local Similarity 100.0%; Pred. No. 2.5e-54;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGGATCTTACTTTTGGGACATGATATACCTTAAACAGGACAGCTT 60
Db 826 TATGAAGCAGGATCTTACTTTTGGGACATGATATACCTTAAACAGGACAGCTT 885
QY 61 GCAAGAGCTGGATTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGA 120
Db 886 GCAAGAGCTGGATTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTTCACTGTGGA 945
QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGACACATGCTAAATGGTAT 180
Db 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGACACATGCTAAATGGTAT 1005
QY 181 CCAGGGTGCAAAATATCTG 198
Db 1006 CCAGGGTGCAAAATATCTG 1023

RESULT 8
AAD03575
ID AAD03575 standard; cDNA; 1752 BP.
XX
AC AAD03575;
XX
DT 19-JUN-2001 (first entry)
XX
DE Human IAP-like protein-3 (ILP-3) cDNA.
XX
KW Human; inhibitor of apoptosis; IAP-like protein-3; ILP-3;
KW chromosome 2q12-q14; transforming growth factor beta receptor; TGFbetaR;
KW c-Jun N-terminal kinase; JNK; gene therapy; osteoarthritis; cytostatic;
KW hypothyroidism; juvenile nephronophthisis; thrombophilia; cancer;
KW colorectal cancer; neonatal purpura fulminans; autoimmune disease;
KW diabetes; multiple sclerosis; neurodegenerative disease;
KW retinal degeneration; ss.
XX
OS Homo sapiens.

XX Key Location/Qualifiers
FH CDS 847..1197
FT /*tag= a
FT /product= "Human inhibitor of apoptosis (IAP)-like protein-3 (hILP-3)"
XX
XX WO200123558-A2.
XX 05-APR-2001.
XX 29-SEP-2000; 2000WO-US26735.
XX 30-SEP-1999; 99US-0157169.
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX Duckett C, Mir SS;
XX WPI: 2001-258135/26.
XX P-PSDB: AAE00359.
XX Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with transforming growth factor beta receptor modulating activity, and the nucleic acids that encode them, useful for treating, e.g. diabetes and multiple sclerosis -
XX
XX Claim 18; Page 87-88; 108pp; English.

The present sequence is human inhibitor of apoptosis (IAP)-like protein-3 (ILP-3) cDNA. The hILP-3 gene is located on chromosome 2q12-q14. ILP-3 comprises a spacer region and a ring finger domain. The ILP interacts with transforming growth factor beta receptor (TGFbetaR) and modulates TGFbetaR activity. ILP-3 also moderately inhibits ILP-1 mediated c-Jun N-terminal kinase (JNK) activation when co-transfected with ILP-1. Such activity decreases or prevents apoptosis in a cell.

CC ILP-3 is used in the area of genetic testing for predisposition to
 CC diseases, such as osteoarthritis, hypothyroidism, juvenile
 CC nephronophthisis, thrombophilia, colorectal cancer and neonatal purpura
 CC fulminans owing to an ILP-3 deletion or mutation. The ILP is also used
 CC in the treatment of diseases associated with abnormal apoptosis such as
 CC cancer, autoimmune diseases, e.g., diabetes and multiple sclerosis and
 CC neurodegenerative diseases including retinal degeneration. The ILP-3
 CC gene is also used in gene therapy for treating patients suffering from
 CC ILP-3 gene deletions or mutations.

XX Sequence 1752 BP; 530 A; 299 C; 385 G; 538 T; 0 other;

Query Match 91.1%; Score 180.4; DB 22; Length 1752;
 Best Local Similarity 94.4%; Pred. No. 9.4e-49;
 Matches 187; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTACTTTGGGACATGGATATCTACTCAGTTAAAGAGCAGCAGCTT 60
 DB 499 TATGAAGCAGCGATCTTACTTTGGGACATGGATATCTACTCAGTTAAAGAGCAGCAGCTT 558
 QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATTAAGTAAAGTCTTTCACCTGTGGA 120
 DB 559 TCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATTAAGTAAAGTCTTTCACCTGTGGA 618
 QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
 DB 619 GGGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGATTAATGGCAT 678
 QY 181 CCAGGGTGCAAAATATCTG 198
 DB 679 CCAGGGTGCAAAATATCTG 696

RESULT 9
 AAT72710

ID AAT72710 standard; DNA; 1988 BP.

XX AAT72710;

DT 16-SEP-1997 (first entry)

XX Mouse inhibitor of apoptosis protein homologue MIHA DNA.

XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
 KW degenerative disease; infectious disease; autoimmune disease;
 KW cancer; gene therapy; diagnosis; ss.

XX Mus musculus.

XX Key Location/Qualifiers
 XX CDS 212..1702
 XX /*tag= a

XX WO9723501-A1.

XX 03-JUL-1997.

XX 20-DEC-1996; 96WO-AU00827.

XX 22-DEC-1995; 95AU-0007275.

XX (AMRA-) AMRAD OPERATIONS PTY LTD.

XX Vaux DL;

XX WPI; 1997-350966/32.

XX P-PSDB; AAW19745.

XX Isolated protein homologues of viral inhibitors of apoptosis - used
 PT to modulate apoptosis for treatment of degenerative, infectious or
 PT autoimmune diseases and cancer

XX Claim 24; Page 44-47; 136pp; English.

XX An isolated nucleic acid molecule (AAT72710) codes for mammalian IAP
 CC homologue A (MIHA) (AAW19745), a murine homologue of baculovirus
 CC inhibitor of apoptosis protein (IAP). It was isolated from a mouse
 CC liver cDNA library on the basis of homology to Orgyia pseudotsugata
 CC polyhedrosis virus IAP BIR and RING finger amino acid motifs.
 CC Animal IAP homologue nucleic acids (see also AAT72711-17) can be used
 CC to produce polypeptides useful in methods for modulating apoptosis
 CC in animal cells, specifically for treatment, by inhibition, of
 CC degenerative and infectious disease or, by promotion, of cancer and
 CC autoimmune disease, and can be used for gene therapy of these
 CC diseases.

XX Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 other;

Query Match 88.2%; Score 174.6; DB 18; Length 1988;
 Best Local Similarity 92.9%; Pred. No. 7.7e-47;
 Matches 183; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTACTTTGGGACATGGATATCTACTCAGTTAAAGAGCAGCAGCTT 60
 DB 1001 TATGAAGCAGCGATCGTTACTTTTGGAAACATGGACATCTCAGTTAAAGAGCAGCAGCTT 1060
 QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATTAAGTAAAGTCTTTCACCTGTGGA 120
 DB 1061 GCAAGAGCTGGATTTATGCTTTAGGTGAAGTGATTAAGTAAAGTCTTTCACCTGTGGA 1120
 QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
 DB 1121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCGAAGTGTAT 1180
 QY 181 CCAGGGTGCAAAATATCT 197
 DB 1181 CCAGGGTGCAAAATATCT 1197

RESULT 10

AAT70839

ID AAT70839 standard; cDNA; 2100 BP.

XX AAT70839;

DT 02-SEP-1997 (first entry)

XX Mouse apoptosis inhibitor m-xiap cDNA.

XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
 KW M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;
 KW ischaemia; myocardial infarction; stroke;
 KW reperfusion injury; toxin-induced liver disease; gene therapy;
 KW diagnosis; ds.

XX Mus sp.

XX Key Location/Qualifiers
 XX CDS 127..1617
 XX /*tag= a

XX WO9706255-A2.

XX 20-FEB-1997.

XX 05-AUG-1996; 96WO-IB01022.

XX 22-DEC-1995; 95US-0576956.

XX 04-AUG-1995; 95US-0511485.

XX (UYOT-) UNIV OTTAWA.

XX Baird S, Korneluk RG, Liston P, Mackenzie AE;

XX WPI; 1997-154262/14.

XX P-PSDB; AAW19584.

XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
 PT of susceptibility to apoptotic disease
 XX Claim 11; Page 78-79; 219pp; English.
 PS Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and
 CC hiap-2 genes (AAT70836-41) respectively code for a new class of
 CC mammalian proteins (AAW1981-86) that are inhibitors of apoptosis
 CC (IAP). The murine xiap gene (for X-linked IAP gene) sequence was
 CC constructed from 12 overlapping clones isolated from a mouse
 CC embryo lambda-gt11 cDNA library and from a mouse FIX II genomic
 CC library using human xiap cDNA as probe. IAP nucleic acids can be
 CC used to express IAP polypeptides in cells and animals to inhibit
 CC apoptosis, and as primers and probes to identify and isolate
 CC additional IAP genes, as well as in methods for treating diseases
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).
 XX Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;
 SQ
 Query Match 87.4%; Score 173; DB 18; Length 2100;
 Best Local Similarity 92.4%; Pred. No. 2.6e-46;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 1 TATGAAGCAGGATCTTTACTTTTGGACATGATATCTCAGTTAACAAGGAGCAGCTT 60
 Db TATGAAGCAGGATCTTTACTTTTGGACATGATATCTCAGTTAACAAGGAGCAGCTT 975
 QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTGCCTTCACTGTGGA 120
 Db GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTGCCTTCACTGTGGA 1035
 QY 121 GGAGGCTAACGTGTTGGAAGCCAGTGAAGACCTTGGGAACACATGCTAAATGGTAT 180
 Db GGAGGCTAACGTGTTGGAAGCCAGTGAAGACCTTGGGAACACATGCTAAATGGTAT 1095
 QY 181 CCAGGTGCAAAATATCT 197
 Db CCAGGTGCAAAATATCT 1112
 RESULT 11
 ABK93872
 ID ABK93872 standard; cdna; 2100 BP.
 XX
 AC ABK93872;
 DT 26-AUG-2002 (first entry)
 XX
 DE Mouse cDNA encoding inhibitor of apoptosis, XIAP.
 XX
 KW Mouse; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Mus sp.
 PN WO200226968-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-CA01379.
 XX
 PR 28-SEP-2000; 2000US-0672717.
 XX
 PA (UYOT-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 PI Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

XX WPI; 2002-479562/51.
 DR P-PSDB; ABG65666..
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for
 PT enhancing apoptosis in a cell, for treating cancer and other
 PT proliferative diseases -
 XX Disclosure; Fig 4; 135pp; English.
 PS
 XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (I) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
 CC cDNA sequence.
 XX
 SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;
 Query Match 87.4%; Score 173; DB 24; Length 2100;
 Best Local Similarity 92.4%; Pred. No. 2.6e-46;
 Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;
 QY 1 TATGAAGCAGGATCTTTACTTTTGGACATGATATCTCAGTTAACAAGGAGCAGCTT 60
 Db TATGAAGCAGGATCTTTACTTTTGGACATGATATCTCAGTTAACAAGGAGCAGCTT 975
 QY 61 GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTGCCTTCACTGTGGA 120
 Db GCAAGAGCTGGATTTATGCTTTAGTGAAGGTGATATAAGTAAAGTGCCTTCACTGTGGA 1035
 QY 121 GGAGGCTAACGTGATTGGAAGCCAGTGAAGACCTTGGGAACACATGCTAAATGGTAT 180
 Db GGAGGCTAACGTGATTGGAAGCCAGTGAAGACCTTGGGAACACATGCTAAATGGTAT 1095
 QY 181 CCAGGTGCAAAATATCT 197
 Db CCAGGTGCAAAATATCT 1112
 RESULT 12
 AAV55041
 ID AAV55041 standard; cdna; 2691 BP.
 XX
 AC AAV55041;
 XX
 DT 13-NOV-1998 (first entry)
 XX
 DE Murine XIAP coding sequence.
 XX
 KW Inhibitor of apoptosis protein; apoptosis enhancer; XIAP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.
 XX
 OS Mus sp.
 FH Location/Qualifiers
 FT Key 672..2162
 FT CDS /*tag= a
 FT /product= XIAP
 XX
 PN WO9835693-A2.

Db 190 CCAGGTGCAAAATATCTG 207

RESULT 14

ABK14677

ID ABK14677 standard; cDNA; 1758 BP.

XX

AC ABK14677;

XX

DT 08-MAY-2002 (first entry)

XX

DE Human inhibitor of apoptosis protein 7 (IAPL7) cDNA.

XX

KW Human; gene; inhibitor of apoptosis 7; IAPL7; cytostatic;

KW antiapoptotic; IAP; apoptosis; antibody; V-Rel; NF-kappaB;

KW chromosome 19; vaccine; gene therapy; hyperproliferative disease;

KW cancer; transgenic animal; ss.

XX

OS Homo sapiens.

XX

PH Key

FT CDS

FT 286..1680

FT /*tag= a

FT /product= "IAPL7 protein"

FT /partial

FT /note= "No start codon shown"

XX

PN WO200210381-A1.

XX

XX

PD 07-FEB-2002.

XX

PE 18-JUL-2001; 2001WO-EP08287.

XX

PR 28-JUL-2000; 2000EP-0116452.

XX

PA (MERE) MERCK PATENT GMBH.

PI Hentsch B;

XX

XX WPI; 2002-188741/24.

DR P-PSDB; AAU75747.

XX

PT New inhibitor of apoptosis proteins and polynucleotides useful in

PT vaccines for inducing an immune response against hyperproliferative

PT diseases e.g. cancer

XX

PS Claim 5; Page 33-35; 41pp; English.

XX

XX This invention relates to the nucleic acid and protein sequences of a

CC novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences

CC have homology to the IAP (inhibitors of apoptosis) gene family which

CC are thought to inhibit proteins by regulating the anti-apoptotic

CC activity of the V-Rel and NF-kappaB family of transcription factors.

CC The gene for IAPL7 is located on human chromosome 19. The nucleic acids

CC of the invention are useful for screening to identify compounds that

CC stimulate or inhibit the function or level of IAPL7, where the

CC identified compounds are useful for treating hyper-proliferative

CC diseases such as cancer. The protein sequences may also be used to

CC identify membrane bound or soluble receptors of IAPL7 by standard

CC receptor binding techniques. Nucleic acids encoding IAPL7, may be used

CC as hybridisation probes for cDNA and genomic DNA, or as primers for

CC nucleic acid amplification reaction and the primers and probes may also

CC be used to isolate full-length cDNAs and genomic clones encoding IAPL7.

CC The nucleic acid sequences are useful as diagnostic reagents for

CC diagnosing a disease or a susceptibility to a disease by detecting

CC mutations in the associated gene. The nucleic acid sequence is useful

CC for chromosome localisation and tissue expression studies and is also

CC useful for producing transgenic animals. The IAPL7 protein sequence may

CC also be used to generate an anti-IAPL7 antibody which is useful in

CC screening methods for detecting the effect of added compounds on the

CC production of mRNA and protein in cells. The sequences of the invention

CC are also useful as vaccines for inducing an immunological response in a

CC mammal. The present sequence represents the cDNA encoding the human

CC Inhibitor of apoptosis 7 (IAP7) protein of the invention.

XX

SQ Sequence 1758 BP; 488 A; 371 C; 470 G; 429 T; 0 other;

Query Match 83.8%; Score 166; DB 24; Length 1758;

Best Local Similarity 89.9%; Pred. No. 4.7e-44;

Matches 178; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCATCTTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60

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Db 979 TATGAAGCCCGCTCATTTACTTTTGGGACATGGATGTACTCGTTAAACAAGGAGCAGCTT 1038

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGAAGTGATAAGTAAGTAACTGCTTTTCACTGTGGA 120

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1039 GCAAGAGCTGGATTTTATGCTATAGTCAAGAGGATAAAGTACAGTCTTTTCACTGTGGA 1098

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 121 GGAGGCTTAAGTGAAGCCAGTCAAGACCTTTGGGAACAACATGCTAAATGGTAT 180

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1099 GGAGGCTTAGCCACTGGAGCCCAAGGAAGATCCTTGGGAACAGCATGCTAAATGGTAT 1158

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 181 CCAGGCTGCAAAATATCTG 198

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 1159 CCAGGCTGCAAAATATCTG 1176

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15

ABK14678

ID ABK14678 standard; cDNA; 1758 BP.

XX

AC ABK14678;

XX

DT 08-MAY-2002 (first entry)

XX

DE Human Inhibitor of apoptosis protein 7 (IAPL7) cDNA #2.

XX

KW Human; gene; inhibitor of apoptosis 7; IAPL7; cytostatic;

KW antiapoptotic; IAP; apoptosis; antibody; V-Rel; NF-kappaB; antibody;

KW chromosome 19; vaccine; gene therapy; hyperproliferative disease;

KW cancer; transgenic animal; ss.

XX

OS Homo sapiens.

XX

PH Key

FT CDS

FT 286..687

FT /*tag= a

FT /product= "IAPL7 protein"

FT /partial

FT /note= "This sequence encodes amino acid

FT residues 1-133 of the protein shown in

FT AAU75747. No start codon shown"

XX

PN WO200210381-A1.

XX

XX 07-FEB-2002.

PD

XX 18-JUL-2001; 2001WO-EP08287.

PF

XX 28-JUL-2000; 2000EP-0116452.

PR

XX (MERE) MERCK PATENT GMBH.

PI Hentsch B;

XX

XX WPI; 2002-188741/24.

DR

XX New inhibitor of apoptosis proteins and polynucleotides useful in

PT vaccines for inducing an immune response against hyperproliferative

PT diseases e.g. cancer

XX

PS Claim 5; Page 36-38; 41pp; English.

XX

XX This invention relates to the nucleic acid and protein sequences of a

CC novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:16:42 ; Search time 24.9219 Seconds
(without alignments)
2436.494 Million cell updates/sec

Title: US-09-654-743-47
Perfect score: 198
Sequence: 1 tatgaagcagcagcttttac.....atccagggtgcaatatctg 198

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	198	100.0	1588	4	US-09-239-867-3
2	198	100.0	2540	2	US-08-511-485-3
3	198	100.0	2540	3	US-09-392-580-1
4	198	100.0	5232	3	US-09-212-971-3
5	198	100.0	5232	3	US-08-800-929A-3
6	198	100.0	5232	4	US-09-617-053A-3
7	173	87.4	2100	2	US-08-511-485-9
8	169.8	85.8	2691	3	US-09-212-971-9
9	169.8	85.8	2691	3	US-08-800-929A-9
10	169.8	85.8	2691	4	US-09-617-053A-9
11	164.4	83.0	711	3	US-09-121-979-3
12	164.4	83.0	711	4	US-09-332-319-3
13	164.4	83.0	1559	4	US-09-239-867-1
14	157.8	79.7	152331	3	US-09-128-155-16
15	131.4	66.4	176373	3	US-09-128-155-17
16	78.6	39.7	2601	4	US-08-569-749-3
17	78.6	39.7	2601	5	PCT-US96-12860-3
18	78.6	39.7	2676	2	US-08-511-485-5
19	78.6	39.7	3076	2	US-09-205-144-1
20	78.6	39.7	6669	3	US-09-212-971-5
21	78.6	39.7	6669	3	US-08-800-929A-5
22	78.6	39.7	6669	4	US-09-617-053A-5
23	74.4	37.6	1435	5	PCT-US95-05922A-1
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30	74.4	37.6	3732	4	US-09-617-053A-7
31	71.2	36.0	2862	4	US-08-569-749-13
32	71.2	36.0	2862	5	PCT-US96-12860-13
33	71.2	36.0	3151	3	US-09-212-971-13
34	71.2	36.0	3151	3	US-08-800-929A-13
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41	32	16.2	522	4	US-08-998-416-160
42	28.4	14.3	736	4	US-09-030-333-7
43	28.4	14.3	1824	4	US-09-030-333-1
44	28.4	14.3	1938	4	US-08-975-762-49
45	28.4	14.3	1938	4	US-09-295-028-49

ALIGNMENTS

RESULT 1
US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-239-867-3

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Gaps	0						
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Db	826	TATGAAGCAGCGGATCTTTACTTTTGGGACATGGATATCTCAGTTTACAAAGGAGCAGCTT	885				
QY	61	GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTCTTTCTACTGTGGA	120				
Db	886	GCAAGAGCTGGATTTTATGCTTTAGGTGAAGGTGATAAAGTCTTTCTACTGTGGA	945				
QY	121	GGAGGGCTTAAGTGGAGCCAGTGAAGACCCCTTGGGAACACATGCTTAATGCTAT	180				
Db	946	GGAGGGCTTAAGTGGAGCCAGTGAAGACCCCTTGGGAACACATGCTTAATGCTAT	1005				
QY	181	CCAGGGTGCAAAATCTCG	198				
Db	1006	CCAGGGTGCAAAATCTCG	1023				
RESULT 2							
US-08-511-485-3							
; Sequence 3, Application US/08511485							
; Patent No. 5919912							
; GENERAL INFORMATION:							
; APPLICANT: Korneluk, Robert G.							
; APPLICANT: Mackenzie, Alexander E.							
; APPLICANT: Baird, Stephen							

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2540 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
US-08-511-485-3

Query Match 100.0%; Score 198; DB 2; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 826 TATGAAGCAGGATCTTTACTTTTGGGACATGATATCTCACTTAACAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGGAAGTGAATGAAGTAAAGTCTTCACTGTGGA 120
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Db 886 GCAAGAGCTGGATTTTATGCTTTAGTGGAAGTGAATGAAGTAAAGTCTTCACTGTGGA 945
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|||||
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QY 181 CCAGGTGCAAAATATCTG 198
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Db 1006 CCAGGTGCAAAATATCTG 1023

RESULT 3
US-09-392-580-1
Sequence 1, Application US/09392580
Patent No. 6087173
GENERAL INFORMATION:
APPLICANT: C. Frank Bennett
APPLICANT: Elizabeth J. Ackermann
APPLICANT: Lex M. Cowser
TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSION
FILE REFERENCE: RTS-0072
CURRENT APPLICATION NUMBER: US/09/392,580
CURRENT FILING DATE: 1999-09-09
NUMBER OF SEQ ID NOS: 47
SEQ ID NO 1
LENGTH: 2540
TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (34)...(1527)
US-09-392-580-1
Query Match 100.0%; Score 198; DB 3; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCTTTACTTTTGGGACATGATATCTCACTTAACAGGAGCAGCTT 60
|||||
Db 826 TATGAAGCAGGATCTTTACTTTTGGGACATGATATCTCACTTAACAGGAGCAGCTT 885
QY 61 GCAAGAGCTGGATTTTATGCTTTAGTGGAAGTGAATGAAGTAAAGTCTTCACTGTGGA 120
|||||
Db 886 GCAAGAGCTGGATTTTATGCTTTAGTGGAAGTGAATGAAGTAAAGTCTTCACTGTGGA 945
QY 121 GGAGGCTAACTGATTGGAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
|||||
Db 946 GGAGGCTAACTGATTGGAGCCCACTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
QY 181 CCAGGTGCAAAATATCTG 198
|||||
Db 1006 CCAGGTGCAAAATATCTG 1023

RESULT 4
US-09-212-971-3
Sequence 3, Application US/09212971B
Patent No. 6107041
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009002
CURRENT APPLICATION NUMBER: US/09/212,971B
CURRENT FILING DATE: 1998-12-16
EARLIER APPLICATION NUMBER: 60/017,354
EARLIER FILING DATE: 1996-04-26
EARLIER APPLICATION NUMBER: 60/030,590
EARLIER FILING DATE: 1996-11-14
EARLIER APPLICATION NUMBER: 08/800,929
EARLIER FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 5232
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (4623)...(4623)
OTHER INFORMATION: n can be any nucleotide
FEATURE:
NAME/KEY: variation
LOCATION: (4622)...(4622)
OTHER INFORMATION: n can be any nucleotide
US-09-212-971-3

Query Match 100.0%; Score 198; DB 3; Length 5232;
Best Local Similarity 100.0%; Pred. No. 2.7e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCAGGATCTTTACTTTTGGGACATGATATCTCACTTAACAGGAGCAGCTT 60
|||||
Db 826 TATGAAGCAGGATCTTTACTTTTGGGACATGATATCTCACTTAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGATTTTACGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120
|||||
Db 886 GCAAGAGCTGATTTTACGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 945
|||||
QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
|||||
Db 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
|||||
QY 181 CCAGGGTGCAAAATATCTG 198
|||||
Db 1006 CCAGGGTGCAAAATATCTG 1023
|||||

RESULT 5

US-08-800-929A-3
; Sequence 3, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bieker-Brady, Kristina
; REGISTRATION NUMBER:
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5232 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Other
; LOCATION: 1...5232
; OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.
US-08-800-929A-3

Query Match 100.0%; Score 198; DB 3; Length 5232;
Best Local Similarity 100.0%; Pred. No. 2.7e-59;

Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 TATGAAGCACGGATCTTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
|||||
Db 826 TATGAAGCACGGATCTTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885
|||||
QY 61 GCAAGAGCTGATTTTACGCTTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120
|||||
Db 886 GCAAGAGCTGATTTTACGCTTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 945
|||||
QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
|||||
Db 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
|||||
QY 181 CCAGGGTGCAAAATATCTG 198
|||||
Db 1006 CCAGGGTGCAAAATATCTG 1023
|||||

RESULT 6

US-09-617-053A-3
; Sequence 3, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (4623)...(4623)
; OTHER INFORMATION: n can be any nucleotide
; NAME/KEY: variation
; LOCATION: (4622)...(4622)
; OTHER INFORMATION: n can be any nucleotide
US-09-617-053A-3

Query Match 100.0%; Score 198; DB 4; Length 5232;
Best Local Similarity 100.0%; Pred. No. 2.7e-59;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCACGGATCTTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 60
|||||
Db 826 TATGAAGCACGGATCTTTTACTTTTGGGACATGGATATACTCAGTTAAACAAGGAGCAGCTT 885
|||||
QY 61 GCAAGAGCTGATTTTATGCTTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 120
|||||
Db 886 GCAAGAGCTGATTTTATGCTTTTAGGTGAAGGTGATAAGTAAAGTCTTTCACTGTGGA 945
|||||
QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
|||||
Db 946 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005
|||||
QY 181 CCAGGGTGCAAAATATCTG 198
|||||
Db 1006 CCAGGGTGCAAAATATCTG 1023
|||||

RESULT 7
US-08-511-485-9
; Sequence 9, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511.485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match 87.4%; Score 173; DB 2; Length 2100;
Best Local Similarity 92.4%; Pred. No. 9.6e-51;
Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGCGATCTTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
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Db 916 TATGAAGCAGCGATCGTTTACTTTTGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 975
|||||

Qy 61 GCAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAGTAAAGTGCTTTTCACTGTGGA 120
|||||
Db 976 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAGTAAAGTGCTTTTCACTGTGGA 1035
|||||

Qy 121 GGAGGGCTAACTGATTGGAAGCCAGTCAGACCCCTGGGACACATGCTTAATGGTAT 180
|||||
Db 1036 GGAGGGCTCAGGATTGGAAGCCAGTCAGACCCCTGGGACACATGCTTAATGGTAT 1095
|||||

Qy 181 CCAGGGTGCAAAATATCT 197
|||||
Db 1096 CCAGGGTGCAAAATACCT 1112
|||||

RESULT 8
US-09-212-971-9
; Sequence 9, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.

; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212.971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017.354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030.590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800.929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-212-971-9

Query Match 85.8%; Score 169.8; DB 3; Length 2691;
Best Local Similarity 91.4%; Pred. No. 1.4e-49;
Matches 180; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

Qy 1 TATGAAGCAGCGATCTTTTACTTTTGGGACATGGATATCTCAGTTAAACAAGGAGCAGCTT 60
|||||
Db 1461 TATGAAGCAGCGATCGTTTACTTTTGGACATGGACATCTCAGTTAAACAAGGAGCAGCTT 1520
|||||

Qy 61 GCAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAGTAAAGTGCTTTTCACTGTGGA 120
|||||
Db 1521 GCAAGAGCTGGATTTATGCTTTTAGGTGAAGGTGATAAGTAAAGTGCTTTTCACTGTGGA 1580
|||||

Qy 121 GGAGGGCTAACTGATTGGAAGCCAGTCAGACCCCTGGGACACATGCTTAATGGTAT 180
|||||
Db 1581 GGAGGGCTCAGGATTGGAAGCCAGTCAGACCCCTGGGACACATGCTTAATGGTAT 1640
|||||

Qy 181 CCAGGGTGCAAAATATCT 197
|||||
Db 1641 CCAGGGTGCAAAATACCT 1657
|||||

RESULT 9
US-08-800-929A-9
; Sequence 9, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 26-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bleker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 2691 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-800-929A-9

Query Match 85.8%; Score 169.8; DB 3; Length 2691;
Best Local Similarity 91.4%; Pred. No. 1.4e-49;
Matches 180; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 TATGAACGACGGATCTTTTACTTTTGGGACATGGATATACCTAGTAAAGGAGCAGCTT 60
|||||
DB 1461 TATGAACGACGGATCGTTACTTTTGGACATGGACATCCCTCAGTTAAAGGAGCAGCTT 1520
|||||

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTCAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
|||||
DB 1521 GCAAGAGCTGGATTTATGCTTTAGGTCAAGGTGATAAAGTAAAGTCTTCACTGTGGA 1580
|||||

QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGACACATGCTAAATGGTAT 180
|||||
DB 1581 GGAGGGCTACGGATTGGAAGCCCAAGTGAAGACCCCTGGGACCATGCTAAATGGTAT 1640
|||||

QY 181 CCAGGGTGCAAAATATCT 197
|||||

DB 1641 CCAGGGTGCAAAATACCT 1657

RESULT 10
US-09-617-053A-9
Sequence 9, Application US/09617053A
Patent No. 6300492
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 2691
TYPE: DNA
ORGANISM: Mus musculus
US-09-617-053A-9

Query Match 85.8%; Score 169.8; DB 4; Length 2691;
Best Local Similarity 91.4%; Pred. No. 1.4e-49;
Matches 180; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 TATGAACGACGGATCTTTTACTTTTGGGACATGGATATACCTAGTAAAGGAGCAGCTT 60
|||||
DB 1461 TATGAACGACGGATCGTTACTTTTGGACATGGACATCCCTCAGTTAAAGGAGCAGCTT 1520
|||||

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
|||||
DB 1521 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 1580
|||||

QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGACACATGCTAAATGGTAT 180
|||||
DB 1581 GGAGGGCTACGGATTGGAAGCCCAAGTGAAGACCCCTGGGACCATGCTAAATGGTAT 1640
|||||

QY 181 CCAGGGTGCAAAATATCT 197
|||||

DB 1641 CCAGGGTGCAAAATACCT 1657

RESULT 11
US-09-121-979-3
Sequence 3, Application US/09121979
Patent No. 6159709
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Holcik, Martin
APPLICANT: Liston, Peter
TITLE OF INVENTION: XIAP IRES AND USES THEREOF
FILE REFERENCE: 07891/021001
CURRENT APPLICATION NUMBER: US/09/121,979
CURRENT FILING DATE: 1998-07-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 3
LENGTH: 711
TYPE: DNA
ORGANISM: Homo sapiens
US-09-121-979-3

Query Match 83.0%; Score 164.4; DB 3; Length 711;
Best Local Similarity 89.4%; Pred. No. 5.9e-48;
Matches 177; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

QY 1 TATGAACGACGGATCTTTTACTTTTGGGACATGGATATACCTAGTAAAGGAGCAGCTT 60
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DB 10 TATGAAGCCCGGCTCATTACTTTTGGGACATGGATGTTACTCCGTCACAAAGAGCAGCTT 69
|||||

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCACTGTGGA 120
|||||
DB 70 GCAAGAGCTGGATTTATGCTTATAGGTCAAGAGGATAAAGTACAGTCTTCACTGTGGA 129
|||||

QY 121 GGAGGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGACACATGCTAAATGGTAT 180
|||||
DB 130 GGAGGGCTAGCCACTGGAAGCCCAAGGAGATCTCTTGGGACATGCTAAATGGTAT 189
|||||

QY 181 CCAGGGTGCAAAATATCTG 198
|||||

DB 190 CCAGGGTGCAAAATATCTG 207
|||||

RESULT 12
US-09-332-319-3
Sequence 3, Application US/09332319
Patent No. 6171821
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Holcik, Martin
APPLICANT: Liston, Peter
TITLE OF INVENTION: XIAP IRES AND USES THEREOF
FILE REFERENCE: 07891/021002
CURRENT APPLICATION NUMBER: US/09/332,319


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; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match      66.4%; Score 131.4; DB 3; Length 176373;
Best Local Similarity 95.7%; Pred. No. 2.1e-35;
Matches 135; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 58 CTTCGAAGAGCTGGATTTTATGCTTTTAGTGGAAGTGATAAAGTAAAGTCTTTCACTGT 117
Db 12549 CTTTCAAGAGCTGGATTTTATGCTTTTAGTGGAAGTGATAAAGTAAAGTCTTTCACTGT 12608

QY 118 GGAGGAGGGCTAAGTATTGGAGCCCGAGTGAAGACCCCTTGGGAACAACATGCTAAATGG 177
Db 12609 GGAGGAGGGCTAAGTATTGGAGCCCGAGTGAAGACCCCTTGGGAACAACATGATAATGG 12668

QY 178 TATCCAGGGTGCAAAATATCTG 198
Db 12669 CATCCAGGGTGTAATAATCTG 12689
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Search completed: April 16, 2003, 00:58:14
Job time : 66.9219 secs

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Result No.	Score	Query Match	Length	DB	ID	Description
1	198	100.0	2404	9	US-09-964-899-38	Sequence 38, Appl
2	198	100.0	2540	9	US-09-201-936-3	Sequence 3, Appli
3	198	100.0	5232	10	US-09-974-592-3	Sequence 3, Appli
4	173	87.4	2100	9	US-09-201-936-9	Sequence 9, Appli
5	169.8	85.8	2691	10	US-09-974-592-9	Sequence 9, Appli
6	157.8	79.7	152331	9	US-10-095-407-16	Sequence 16, Appl
7	131.4	66.4	176373	9	US-10-095-407-17	Sequence 17, Appl
8	78.6	39.7	2676	9	US-09-201-936-5	Sequence 5, Appli
9	78.6	39.7	3076	9	US-09-954-531-16	Sequence 16, Appl
10	78.6	39.7	3076	10	US-09-934-456-1635	Sequence 1635, Ap
11	78.6	39.7	6669	10	US-09-974-592-5	Sequence 5, Appli
12	74.4	37.6	2580	9	US-09-201-936-7	Sequence 7, Appli
13	74.4	37.6	3532	10	US-09-880-107-3354	Sequence 3354, Ap
14	74.4	37.6	3732	10	US-09-974-592-7	Sequence 7, Appli
15	71.2	36.0	3151	10	US-09-974-592-13	Sequence 13, Appl
16	70.6	35.7	2676	10	US-09-974-592-11	Sequence 11, Appl
17	69.6	35.2	2416	9	US-09-201-936-41	Sequence 41, Appl
18	69	34.8	2416	9	US-09-201-936-39	Sequence 39, Appl
19	59	29.8	3773	9	US-10-041-859-1	Sequence 1, Appli

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.


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RESULT 2
US-09-201-936-3
; Sequence 3, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201.936
; EARLIER FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011.356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576.956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511.485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3

Query Match          100.0%; Score 198; DB 9; Length 2540;
Best Local Similarity 100.0%; Pred. No. 7.7e-56;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTACTAGTTAAACAGGAGCAGCTT 60
   |||||||
DB 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTACTAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCTACTGTGGA 120
   |||||||
DB 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCTACTGTGGA 945

QY 121 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
   |||||||
DB 946 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTCAAAATATCTG 198
   |||||||
DB 1006 CCAGGGTCAAAATATCTG 1023

RESULT 3
US-09-974-592-3
; Sequence 3, Application US/09974592
; Patent No. US2002012012A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974.592
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; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: 4623
; OTHER INFORMATION: n can be any nucleotide
; NAME/KEY: variation
; LOCATION: 4622
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-3

Query Match          100.0%; Score 198; DB 10; Length 5232;
Best Local Similarity 100.0%; Pred. No. 1.1e-55;
Matches 198; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTACTAGTTAAACAGGAGCAGCTT 60
   |||||||
DB 826 TATGAAGCAGCGATCTTTACTTTTGGGACATGGATATCTACTAGTTAAACAGGAGCAGCTT 885

QY 61 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCTACTGTGGA 120
   |||||||
DB 886 GCAAGAGCTGGATTTATGCTTTAGGTGAAGGTGATAAGTAAAGTCTTTCTACTGTGGA 945

QY 121 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 180
   |||||||
DB 946 GGAGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGGTAT 1005

QY 181 CCAGGGTCAAAATATCTG 198
   |||||||
DB 1006 CCAGGGTCAAAATATCTG 1023

RESULT 4
US-09-201-936-9
; Sequence 9, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201.936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011.356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576.956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511.485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9

Query Match          87.4%; Score 173; DB 9; Length 2100;
Best Local Similarity 92.4%; Pred. No. 1.5e-47;
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Matches 182; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTACTTTGGGACATGGATATACTAGTTAAACAAGGAGCAGCTT 60
|||||
Db 916 TATGAAGCAGCGATCGTTACTTTGGGACATGGATATACTAGTTAAACAAGGAGCAGCTT 975
|||||

QY 61 GCAAGAGCTGGATTATCTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACCTGTGGA 120
|||||
Db 976 GCAAGAGCTGGATTATCTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACCTGTGGA 1035
|||||

QY 121 GGAGGGCTCACTGATTTGAAGCCCAAGTGAAGACCCCTTGGGACAAACATGCTAAATGGTAT 180
|||||
Db 1036 GGAGGGCTCACTGATTTGAAGCCCAAGTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT 1095
|||||

QY 181 CCAGGGTCAAAATATCT 197
|||||

Db 1096 CCAGGGTCAAAATACCT 1112
|||||

RESULT 5

US-09-974-592-9

; Sequence 9, Application US/09974592

; Patent No. US20020120121A1

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G

; APPLICANT: Mackenzie, Alexander E

; APPLICANT: Liston, Peter

; APPLICANT: Baird, Stephen

; APPLICANT: Tsang, Benjamin K

; APPLICANT: Pratt, Christine

; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND

; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

; FILE REFERENCE: 07891/009004

; CURRENT APPLICATION NUMBER: US/09/974,592

; CURRENT FILING DATE: 2001-10-09

; PRIOR APPLICATION NUMBER: US 09/617,053

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: US 08/800,929

; PRIOR FILING DATE: 1997-02-13

; NUMBER OF SEQ ID NOS: 17

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 9

; LENGTH: 2691

; TYPE: DNA

; ORGANISM: Mus musculus

US-09-974-592-9

Query Match

Best Local Similarity 85.8%; Score 169.8; DB 10; Length 2691;

Matches 180; Conservative 0; Mismatches 17; Indels 0; Gaps 0;

QY 1 TATGAAGCAGCGATCTTACTTTGGGACATGGATATACTAGTTAAACAAGGAGCAGCTT 60

Db 1461 TATGAAGCAGCGATCGTTACTTTGGGACATGGATATACTAGTTAAACAAGGAGCAGCTT 1520

QY 61 GCAAGAGCTGGATTATCTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACCTGTGGA 120

Db 1521 GCAAGAGCTGGATTATCTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACCTGTGGA 1580

QY 121 GGAGGGCTCACTGATTTGAAGCCCAAGTGAAGACCCCTTGGGACAAACATGCTAAATGGTAT 180

Db 1581 GGAGGGCTCACTGATTTGAAGCCCAAGTGAAGACCCCTTGGGACCAACATGCTAAATGGTAT 1640

QY 181 CCAGGGTCAAAATATCT 197

Db 1641 CCAGGGTCAAAATACCT 1657

RESULT 6

US-10-095-407-16/c

; Sequence 16, Application US/10095407

; Patent No. US20020164330A1

; GENERAL INFORMATION:

; APPLICANT: Pan, Yaog

; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

; FILE REFERENCE: 09404/052001

; CURRENT APPLICATION NUMBER: US/10/095,407

; CURRENT FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/091,650

; PRIOR FILING DATE: 1998-07-02

; PRIOR APPLICATION NUMBER: US 60/054,646

; PRIOR FILING DATE: 1997-08-04

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 16

; LENGTH: 152331

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)-(152331)

; OTHER INFORMATION: n = A,T,C or G

US-10-095-407-16

Query Match

Best Local Similarity 79.7%; Score 157.8; DB 9; Length 152331;

Matches 179; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 1 TATGAAGCAGCGATCTTACTTTGGGACATGGATATACTAGTTAAACAAGGAGCAGCTT 60

Db 3298 TATGAAGCAGCGATCATTTACTTTGGGATGTGGATATATTACGTTAAACAAGGAGCAGCTT 3239

QY 61 GCAAGAGCTGGATTATCTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACCTGTGGA 120

Db 3238 TCAAGAGCTGGATTATCTTTAGGTGAAGGTGATAAGTAAAGTGTCTTTCACCTGTGGA 3179

QY 121 GGAGGGCTCACTGATTTGAAGCCCAAGTGAAGACCCCTTGGGACAAACATGCTAAATGGTAT 180

Db 3178 GGGGGGCTCACTGATTTGAAGCCCAAGTGAAGACCCCAAGTGAAGTAAATGGGAT 3120

QY 181 CCAGGGTCAAAATATCTG 198

Db 3119 CCANGGTGTAATATCTG 3102

RESULT 7

US-10-095-407-17

; Sequence 17, Application US/10095407

; Patent No. US20020164330A1

; GENERAL INFORMATION:

; APPLICANT: Pan, Yaog

; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY

; FILE REFERENCE: 09404/052001

; CURRENT APPLICATION NUMBER: US/10/095,407

; CURRENT FILING DATE: 2002-03-11

; PRIOR APPLICATION NUMBER: US 60/091,650

; PRIOR FILING DATE: 1998-07-02

; PRIOR APPLICATION NUMBER: US 60/054,646

; PRIOR FILING DATE: 1997-08-04

; NUMBER OF SEQ ID NOS: 18

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 17

; LENGTH: 176373

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc_feature

; LOCATION: (1)-(176373)

; OTHER INFORMATION: n = A,T,C or G

US-10-095-407-17

Query Match

Best Local Similarity 66.4%; Score 131.4; DB 9; Length 176373;

Matches 179; Conservative 0; Mismatches 18; Indels 1; Gaps 1;


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; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: Patent in version 3.0
; SEQ ID NO: 1635
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-954-456-1635

Query Match      39.7%; Score 78.6; DB 10; Length 3076;
Best Local Similarity 68.8%; Pred. No. 4.6e-16;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 42 AGTTAACAGGAGCAGCTTGCAGAGCTGGATTATGCTTTAGGTGAAGGTGATAAAGT 101
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1534 AGTTAATCCTGACGAGCTTGCAGAGCTGGATTATGCTTTTATTATGGTAAACAGTGATGT 1593

QY 102 AAAGTGCTTCTACTGTGGAGGAGGCTAACTGATTGGAAGCCAGTGAAGACCCCTTGGGA 161
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1594 CAAATGCTTTTCTGTGATGGTGGAGCTCAGGTGCTGGGAATCGGAGATGATCCATGGGT 1653

QY 162 ACAACATGCTAAATGCTATCCAGGCTGCAAAATATCTG 198
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1654 TCAACATGCCAAGTGTTCCTCAAGGTGTGAGTACTTG 1690

RESULT 11
US-09-974-592-5
; Sequence 5, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5
; LENGTH: 6669
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (3677)...(3951)
; OTHER INFORMATION: n can be any nucleotide
US-09-974-592-5

Query Match      39.7%; Score 78.6; DB 10; Length 6669;
Best Local Similarity 68.8%; Pred. No. 6.6e-16;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 42 AGTTAACAGGAGCAGCTTGCAGAGCTGGATTATGCTTTTATTATGGTGAAGGTGATAAAGT 101
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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Db 5030 AGTTAATCCTGACGAGCTTGCAGAGTGCAGGTTTTTATTATGTTGGTAAACAGTGATGT 5089
QY 102 AAAGTGCTTCTACTGTGGAGGAGGCTTACTACTGATTGGAAGCCAGTGAAGACCCCTTGGGA 161
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5090 CAAATGCTTTTCTGTGATGGTGGAGCTCAGGTGTTGGGGAATCTGGAGATGATCCATGGGT 5149
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 162 ACAACATGCTAAATGCTATCCAGGCTGCAAAATATCTG 198
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 5150 TCAACATGCCAAGTGTGTTTCCAAGGTGTGAGTACTTG 5186
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 12
US-09-201-936-7
; Sequence 7, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 7
; LENGTH: 2580
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2412)...(2412)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-7

Query Match      37.6%; Score 74.4; DB 9; Length 2580;
Best Local Similarity 62.2%; Pred. No. 1.1e-14;
Matches 117; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 11 GGATCTTTACTTTTGGGACATGATATACCTCAGTTAAACAAGGAGCAGCTTGCAAGAGCTG 70
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1058 GAACATTTATGTACTGGCCATCTAGTGTTCAGCTTCAGCTTGAGAGCTTGCAAGTCTG 1117
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 71 GATTTTATGCTTTAGGTGAAGGTGATAAAGTAAAGTCTTCTACTGTGGAGGAGGGCTAA 130
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1118 GTTTTATTTATGTGGTCCGAATGATGATGTCRAATGCTTTGTTGTGATGGTGGCTTGA 1177
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 131 CTGATTGGAAGCCAGTGAAGACCCCTTGGGAACAACATGCTAAATGCTATCCAGGGTGA 190
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1178 GGTGTTGGGAATCTGGAGATGATCCATGGTGGTAGAACATGCCAAGTGTTCCTCAAGGTGTG 1237
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 191 AATATCTG 198
      |||||
Db 1238 AGTTCTTG 1245
      |||||

RESULT 13
US-09-880-107-3354
; Sequence 3354, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.

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; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880.107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3334
; LENGTH: 3532
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 U37547
; US-09-880-107-3354

Query Match      37.6%; Score 74.4; DB 10; Length 3532;
Best Local Similarity 62.2%; Pred. No. 1.2e-14;
Matches 117; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 11 GGATCTTTACTTTTGGGACATGGATATACCTCAGTTAAACAAGGAGCAGCTTGAAGAGCTG 70
DB 1980 GAACATTTATGTTAGTGGCCATCTAGTGTCCAGTTCAGCTGAGCAGCTTGAAGTGTG 2039
QY 71 GATTTTATGCTTTAGTGAAGTGATATAAGTAAAGTCTTTTCACTGTGGAGGAGGCTAA 130
DB 2040 GTTTTATATGTTGGTGGCGCAATGATGTCAAAATGCTTTTGTGTGATGGTGGCTTGA 2099
QY 131 CTGATTGGAAGCCCATGAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGCTGA 190
DB 2100 GGTGTTGGAACTCGAGATGATCCATGGGTAGACATGCCCAAGTGGTTTCCAAGGTGTG 2159
QY 191 AATATCTG 198
DB 2160 AGTTCTTG 2167

RESULT 14
US-09-974-592-7
; Sequence 7, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974.592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 3732
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-09-974-592-7

Query Match      37.6%; Score 74.4; DB 10; Length 3732;
Best Local Similarity 62.2%; Pred. No. 1.3e-14;
Matches 117; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 11 GGATCTTTACTTTTGGGACATGGATATACCTCAGTTAAACAAGGAGCAGCTTGAAGAGCTG 70
DB 1578 GGACATTTCTGTACTGCGCCACCTAGTGTCTCTGTTCAAGCCGAGCAGCTTGAAGTGTG 1637
QY 71 GATTTTATGCTTTAGTGAAGTGATATAAGTAAAGTCTTTTCACTGTGGAGGAGGCTAA 130
DB 1638 GATTTTATGCTTTAGTGAAGTGATATAAGTAAAGTCTTTTCACTGTGGAGGAGGCTAA 1697
QY 131 CTGATTGGAAGCCCATGAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGCTGA 190
DB 1698 GATGTTGGGAACCTGGAGATGATCCCTGGTATAGAACACACGCCCAATGGTTTCCAAGGTGTG 1757
QY 191 AATATCTG 198
DB 1758 AGTTCTTG 1765

Query Match      36.0%; Score 71.2; DB 10; Length 3151;
Best Local Similarity 61.2%; Pred. No. 1.3e-13;
Matches 115; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

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QY 71 GATTTTATGCTTTAGTGAAGTGATATAAGTAAAGTCTTTTCACTGTGGAGGAGGCTAA 130
DB 1638 GATTTTATGCTTTAGTGAAGTGATATAAGTAAAGTCTTTTCACTGTGGAGGAGGCTAA 1697
QY 131 CTGATTGGAAGCCCATGAGACCCCTTGGGAACAACATGCTAAATGGTATCCAGGCTGA 190
DB 1698 GATGTTGGGAACCTGGAGATGATCCCTGGTATAGAACACACGCCCAATGGTTTCCAAGGTGTG 1757
QY 191 AATATCTG 198
DB 1758 AGTTCTTG 1765

Search completed: April 16, 2003, 01:03:10
Job time : 90.6094 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:12:47 ; Search time 947.375 seconds
(without alignments)
3384.833 Million cell updates/sec

Title: US-09-654-743-47
Perfect score: 198
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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EST:
1: em_estba:
2: em_esthum:
3: em_estin:
4: em_estnu:
5: em_estov:
6: em_estpl:
7: em_estro:
8: em_etc:
9: gb_esti:
10: gb_est2:
11: gb_etc:
12: gb_est3:
13: gb_est4:
14: gb_est5:
15: em_estfun:
16: em_estom:
17: gb_gss:
18: em_gss_hum:
19: em_gss_inv:
20: em_gss_pln:
21: em_gss_vrt:
22: em_gss_fun:
23: em_gss_mam:
24: em_gss_mus:
25: em_gss_other:
26: em_gss_pro:
27: em_gss_rod:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
c 1	157.4	79.5	628	9	AI573382
2	114	57.6	1177	14	BM805359
3	112	56.6	536	9	AU123207
4	104.4	52.7	716	10	AV706807
5	100.2	50.6	318	12	BF559610
6	99	50.0	617	10	BB663325

7	94.4	47.7	504	10	BB650856
8	91.6	46.3	566	13	BM220130
9	91.6	46.3	584	14	BO552032
10	87	43.9	420	17	AQ011995
11	78.6	39.7	341	10	AW375598
12	78.6	39.7	354	10	AW375594
13	78.6	39.7	402	10	AW846507
14	78.6	39.7	531	10	AW375599
15	78.6	39.7	532	10	AW846425
16	78.6	39.7	546	10	AW846421
17	78.6	39.7	571	10	AW375649
18	78.6	39.7	582	10	AW375648
19	78.6	39.7	590	10	BE268377
20	78.6	39.7	621	10	AW375648
21	78.6	39.7	680	10	AW375625
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23	78.4	39.6	289	10	BE506790
24	74.4	37.6	441	13	BM312708
25	74.4	37.6	563	9	AA702174
26	74.4	37.6	652	10	AW704923
27	74.4	37.6	851	13	BI253303
28	74.4	37.6	896	14	BO439248
29	74.4	37.4	354	9	AA34707
30	73.4	37.1	567	13	BI961039
31	73.4	37.1	889	14	BO720079
32	71.2	36.0	298	12	BF016190
33	71.2	36.0	780	13	BI771720
34	70.6	35.7	323	12	BE847058
35	70.6	35.7	385	12	BE851680
36	70.6	35.7	557	9	AA197349
37	70	35.4	506	13	BM126304
38	69.6	35.2	395	9	AI552965
39	69.4	35.1	302	14	R83677
40	68.6	34.6	673	13	BJ045197
41	68	34.3	286	9	AA473594
42	66.6	33.6	592	13	BJ059822
43	65.4	33.0	423	12	BF325539
44	65	32.8	584	10	AW375608
45	65	32.8	645	10	AW375611

ALIGNMENTS

RESULT 1
AI573382/c
LOCUS
DEFINITION
mm83e12.x1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
IMAGE:550702 3' similar to TR:Q60989 Q60989 MIHA. ; mRNA sequence.
AI573382
ACCESSION
VERSION
KEYWORDS
SOURCE
EST.
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 628)
REFERENCE
AUTHORS
Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person,
B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter,
E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R.,
Waterston, R. and Wilson, R.
TITLE
The WashU-NCI Mouse EST Project 1999
JOURNAL
COMMENT
Unpublished (1999)
Contact: Marra M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@watson.wustl.edu
This clone is available royalty-free through LLNL ; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Possible reversed clone: similarity on wrong strand

BB650856	BB650856
BM220130	C0935E08-
BO552032	H4013A06-
AQ011995	HS_2190.A
AW375598	QVO-CT017
AW375594	QVO-CT017
AW846507	QVO-CT017
AW846425	QVO-CT017
AW846421	QVO-CT017
AW375649	QVO-CT017
AW375648	QVO-CT017
BE268377	601124994
AW375625	QVO-CT017
BO652590	AGENCOURT
BE506790	db87908.Y
BM312708	lg78a10.Y
AA702174	z191908.S
AV704923	AV704923
BI253303	602973538
BO439248	AGENCOURT
AA34707	EST63004
BI961039	MONOL_5_C
BO720079	AGENCOURT
BF016190	UY32A08.Y
BI771720	603058472
BE847058	uw23A06.Y
BE851680	uw99B07.Y
AA197349	mu21C08.F
BM126304	1f04609.Y
AI552965	vg63h10.Y
R83677	vp16f10.r1
BJ045197	BJ045197
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BF325539	C40-AN000
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FEATURES
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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_image="550702"
/clone_lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/note="Organ: blood; Vector: pBluescript SK-; Site.1:
ECORI; Site.2: XhoI; Cloned unidirectionally. Primer:
Oligo dT. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAACTGGCAGAG
3' -3' adaptor sequence: 5' CTCGAGTTTCTTTTCTTTTCTTTT 3"
BASE COUNT 163 a 137 c 115 g 211 t 2 others
ORIGIN
Query Match 79.5%; Score 157.4; DB 9; Length 628;
Best Local Similarity 90.4%; Pred. No. 4e-41;
Matches 178; Conservative 0; Mismatches 18; Indels 1; Gaps 1;

QY 1 TATGAAGCAGGATCTTTTCTTTGGACATGATATACCTAGTTAAACAGGAGCAGCTT 60
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Db 604 TATGAAGCAGGATCTTTTCTTTGGACATGATATACCTAGTTAAACAGGAGCAGCTT 545
|||||
QY 61 GCAAGAGCTGGATTTATGCTTTTAGTGAAGTGATGAATGAAGTCTTTTCTACTGTGGA 120
|||||
Db 544 GCAAGAGCT-GATTTATGCTTTTAGTGAAGTGATGAATGAAGTCTTTTCTACTGTGGA 486
|||||
QY 121 GGAGGCTACTGATTTGGAGCCAGTGAGACCCCTTGGAGCAACATGCTAAATGGTAT 180
|||||
Db 485 GGAGGCTACCGGATTTGGAGCCAGTGAGACCCCTTGGAGCAACATGCTAAATGGTAT 426
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QY 181 CCAGGTGCAATATCT 197
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Db 425 NCAGGTGCAATATCT 409
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RESULT 2
LOCUS BM805359
DEFINITION AGENCOURT_6499731 NIH_MGC_124 Homo sapiens cDNA clone IMAGE:5728685
5', mRNA sequence.
ACCESSION BM805359
VERSION BM805359.1 GI:19122182
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1177)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-f@mail.nih.gov
Tissue Procurement: Invitrogen
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM12724 row: m column: 06
High quality sequence stop: 409.
Location/Qualifiers
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/clone_image="5728685"
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/lab_host="DH10B"
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age 27. Library is oligo-dT primed and directionally
cloned (EcoRV site is destroyed upon cloning). Average
insert size 1.4 kb, insert size range 0.9-4 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 012."
BASE COUNT 284 a 362 c 221 g 310 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 1.4e-26;
Matches 114; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 85 GGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGAGGAGGCTAACTGATTGGAAGCCC 144
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Db 142 GGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGAGGAGGCTAACTGATTGGAAGCCC 201
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QY 145 AGTGAAGACCTTGGGAACAACATGCTAAATGATATCCAGGGTGCAATATCTG 198
|||||
Db 202 AGTGAAGACCTTGGGAACAACATGCTAAATGATATCCAGGGTGCAATATCTG 255
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RESULT 3
LOCUS AU123207
DEFINITION AU123207 NT2RM1 Homo sapiens cDNA clone NT2RM1000921 5', mRNA
sequence.
ACCESSION AU123207
VERSION AU123207.1 GI:10947923
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 536)
Ota.T., Nishikawa.T., Suzuki.Y., Kawai.Y., Ishii.S., Saito.K.,
Nakamura.Y., Nagai.T., Sugano.S. and Isogai.T.
HRI human cDNA project (Ota.T., Nishikawa.T., Suzuki.Y., Kawai.Y.,
Ishii.S., Saito.K., Nakamura.Y., Nagai.T., Sugano.S., Isogai.T.)
Unpublished (2000)
Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
Tel: 81-438-52-3975
Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5' - & 3' - end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
FEATURES
Location/Qualifiers
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precursor cells"
BASE COUNT 172 a 105 c 126 g 124 t 9 others
ORIGIN
Query Match 56.8%; Score 112; DB 9; Length 536;
Best Local Similarity 98.2%; Pred. No. 4.1e-26;
Matches 112; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 85 GGTGAAGTGATAAAGTAAAGTCTTTCACTGTGGAGGAGGCTAACTGATTGGAAGCCC 144
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VERSION	BF659610.1	GI:11924744
KEYWORDS	EST.	
SOURCE	house mouse.	
ORGANISM	Mus musculus	
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	

TITLE
JOURNAL
COMMENT

Db 168 TTGGAAGCCAAAGTGAAGACCTTTGGGAACAGCAGTGGTGAAGTACCAGGGTGCAATA 227

Qy 195 TCT 197

Db 228 CCT 230

RESULT 7

BB650856

LOCUS

DEFINITION BB650856 RIKEN full-length enriched, 0 day neonate cerebellum Mus musculus cDNA clone C230036005 5', mRNA sequence.

ACCESSION BB650856.1 GI:16485110

VERSION

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Arakawa,T., Carninci,P., Fukuda,Y., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

COMMENT Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Konodo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
e mouse tissues.

FEATURES

source

Location/Qualifiers

1..504

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="C230036005"

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/dev_stage="0 day neonate"

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RESULT 7

BB650856

LOCUS

DEFINITION BB650856 RIKEN full-length enriched, 0 day neonate cerebellum Mus musculus cDNA clone C230036005 5', mRNA sequence.

ACCESSION BB650856.1 GI:16485110

VERSION

KEYWORDS

SOURCE house mouse.

ORGANISM Mus musculus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

AUTHORS Arakawa,T., Carninci,P., Fukuda,Y., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Nomura,K., Ohno,M., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.

TITLE RIKEN Mouse ESTs (Arakawa,T., et al. 2001)

COMMENT Unpublished (2001)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes. Genome Res. 10 (10), 1617-1630 (2000)
wagi,K., Fujiwara,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer. Genome Res. 10 (11), 1757-1771 (2000)
Konno,H., Fukunishi,Y., Shibata,K., Itoh,M., Carninci,P., Sugahara,Y. and Hayashizaki,Y.
Computer-based methods for the mouse full-length cDNA encyclopedia: real-time sequence clustering for construction of a nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
Konodo,S., Shinagawa,A., Saito,T., Kiyosawa,H., Yamanaka,I., Aizawa,K., Fukuda,S., Hara,A., Itoh,M., Kawai,J., Shibata,K. and Hayashizaki,Y.
Computational Analysis of Full-Length Mouse cDNAs Compared with Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
Please visit our web site (<http://genome.gsc.riken.go.jp>) for further details.
e mouse tissues.

FEATURES

source

Location/Qualifiers

1..504

/organism="Mus musculus"

/db_xref="taxon:10090"

/clone="C230036005"

/clone_lib="RIKEN full-length enriched, 0 day neonate cerebellum"

/tissue_type="cerebellum"

/dev_stage="0 day neonate"

/lab_host="nhi01"

[illegible][illegible][illegible]

National Institute on Aging/National Institutes of Health 333 Cassell Drive, Suite 3000, Baltimore, MD 21224-6820, USA Email: cdna@lgsun.grc.nia.nih.gov This clone set has been freely distributed to the community. Please visit http://lgsun.grc.nia.nih.gov/cDNA/NIA7_4k.html for details. Plate: H4013 row: A column: 06 Seq primer: -21M13 Forward High quality sequence stop: 584 POLYA=Yes.	Location/Qualifiers 1. .584 /organism="Mus musculus" /strain="C57BL/6"
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/sex="mixed"
/dev_stage="mixed"
/lab_host="DH10B"
/notes="Vector: pSPOT1; Site_1: SalI; Site_2: NotI; This
clone is among a rearranged set of 7,407 clones from more
than 20 cDNA libraries."
BASE COUNT 189 a 125 c 86 g 184 t
ORIGIN
Query Match 46.3%; Score 91.6; DB 14; Length 584;
Best Local Similarity 91.5%; Pred. No. 2.5e-19;
Matches 97; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 82 TTAGTGAAGGTGATAAGTAAAGTCTTCACTGTGAGGAGGCTCAACTGATTGGAAG 141
DB 260 TTAGTGAAGGCGATAAAGTGAAGTCTTCACTGTGAGGAGGCTCAAGGATTGGAAG 201
QY 142 CCAGTGAAGCCCTTGGCAACATGCTAAATGGTATCCAGGCT 187
DB 200 CCAAGTGAAGCCCTTGGCAACATGCTGAAGTGGTACCAGGCT 155

RESULT 10
A0011995/c
LOCUS
DEFINITION HS_2190_AL_MR_G12 CIT Approved Human Genomic Sperm Library D Homo
sapiens genomic clone Plate=2190 Col=23 Row=M, DNA sequence.
ACCESSION A0011995
VERSION A0011995.1 GI:3171671
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 420)
AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 9380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Sequence Tagged Connector
Plate: 2190 row: M column: 23
Class: BAC ends
High quality sequence stop: 420.
Location/Qualifiers
1..420
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/clone_lib="CIT Approved Human Genomic Sperm Library D"
/sex="male"
/notes="Organ: sperm; Vector: pBelOBAcl1; BAC Clones in
E-Coli DH10B"
BASE COUNT 98 a 93 c 73 g 156 t
ORIGIN
Query Match 43.9%; Score 87; DB 17; Length 420;
Best Local Similarity 94.7%; Pred. No. 6.8e-18;
Matches 90; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 104 AGTGCTTTCACTGTGGAGGAGGCTTAAGTATTGAAGCCAGTGAAGACCTTTGGGAAC 163
DB 420 AGTGCTTTCACTGTGGAGGAGGCTTAAGTATTGAAGCCAGTGAAGACCTTTGGGAAC 361
QY 164 AACATGCTAAATGTTATCCAGGGTCAAAATATCTG 198
DB 360 AACATGATAAATGATCCAGGGTGTAAATATCTG 326

RESULT 11
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LOCUS
DEFINITION QV0-CT0179-300999-024-f08 CT0179 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW375598
VERSION AW375598.1 GI:6880161
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 341)
AUTHORS HCGP http://www.ludwig.org.br/ORESTES.
TITLE The FAPESP/LICR Human Cancer Genome Project
JOURNAL Unpublished (1999)
COMMENT Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl-QV0&t2-QV0-CT0179-
300999-024-f08&t3-1999-09-30&t4=1)
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High quality sequence stop: 341.
Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="CT0179"
/dev_stage="Adult"
/notes="Organ: colon; Vector: puc18; Site_1: SmaI; Site_2:
SmaI; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the puc 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."
BASE COUNT 91 a 70 c 83 g 97 t
ORIGIN
Query Match 39.7%; Score 78.6; DB 10; Length 341;
Best Local Similarity 68.8%; Pred. No. 3.7e-15;
Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;

QY 42 AGTTAAACAGGAGCAGCTTGAAGAGCTGGATTATTTAGTGAAGGTGAAGTAAAGT 101
DB 80 AGTTAACTCTGAGCAGCTTGAAGAGCTGGGTTTATTATGTGGTAAACAGTGAATGAT 139
QY 102 AAAGTGCTTCACTGTGGAGGAGGCTAACTGATTGGAGCCCACTGAAGACCCCTTGGGA 161
DB 140 CAATGCTTTGCTGTGATGGTGGACTCAGGTGTTGGGAATCTGGAGATGATCCATGGT 199
QY 162 ACAACATGCTAAATGGTATCCAGGGTGCATAATATCTG 198
DB 200 TCACATGCCAAGTGGTTTCCAAAGGTGTGAGTACTTG 236

RESULT 12

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REFERENCE	TITLE
1. (bases 1 to 402)	
Dias Neto E., Garcia Correa R., Verjovsky-Almeida S., Briones M.R., Nagai M.A., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F., Goldman G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H., Brustein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and Simpson A.J.	Shotgun sequencing of the human transcriptome with ORF expressed

JOURNAL
MEDLINE
COMMENT

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br

This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL (<http://www.ludwig.org.br/scripts/gethtml2.pl?l1=622-QV0-CT0179-240>).

300-175-h08&t3+2000-03-24&t4=1)
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High quality sequence start: 6
High quality sequence stop: 401.

FEATURES	source
Location/Qualifiers	1. 402
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/clone_lib="CT0179"
/dev_stage="Adult"

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/note="Organ: colon; Vector: puc18; Site1: Sma1; Site2: Sma1; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 1995-01-12) into the puc18 vector using the same restriction profiles

716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low

BASE COUNT	stringency conditions."	
117 a	81 C	114 t
	90 g	
ORIGIN		

Query Match	39.7%	Score 78.6;	DB 10;	Length 402;
Best Local Similarity	58.8%	Pred. No. 4e-15;		
Matches 108. Conservative		0: Mismatches	49:	Gaps 0
			Indels	0:

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		127	AGTTAACTCCTGAGCAGCTTGCAGTGCGGGTTTTATTATGTGGGTAAACAGTGATGATGT	186
Db				
		102	AAAGTGCCTTTCACCTGTGCAGGAGGGCTTAACGTATTGGAAAGCCCAAGTGAACACCTTGGCA	161
Ov				

D_b

102 AAAGGCGTTCACGTGGAGGAGGCTAACCTGATTTGGAGCCGATGATGATGATGAT
187 CAATGCTTTTGCTGTGATGGTGACTCAGGTGTTGGGAATCTGGAGATGATCCATGGGT

Qy 162 ACAACATCTAAATGGTATCCAGGGTGCAAAATATCTG 198
DB 247 TCAACATGCCCAAGTGGTTTCCAGGTGCGAGTACTTG 283

RESULT 14

LOCUS	531 bp	linear	EST 04-FEB-2000
AW375599			
DEFINITION	QV0-CT0179-300999-024-g04	CT0179 Homo sapiens cDNA,	mRNA sequence.

ACCESSION AW375599
VERSION AW375599.1 GI:6880162
KEYWORDS EST.

SOURCE	ORGANISM	
human.	Homo sapiens	
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		

Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Hominidae; Homo.
 1 (bases 1 to 531)
 HCGP <http://www.ludwig.org.br/ORESTES>.
 AUTHORS
 REFERENCE

TITLE The FAPESP/LICR Human Cancer Genome Project

JOURNAL
COMMENT

Unpublished (1999)
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-CT0179-
300999-024-g04&t3=1999-09-30&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 531.

FEATURES
source

Location/Qualifiers
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/db_xref="taxon:9606"
/clone_lib="CT0179"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site_1: Sma1; Site_2:
Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 158 a 108 c 121 g 144 t

Query Match 39.7%; Score 78.6; DB 10; Length 531;
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Matches 108; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 42 AGTTAACAAGGAGCAGCTTGCAGAGCTGGATTATGCTTTAGTGAAGGTGATAAAGT 101
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Db 139 AGTTAATCTCGAGCAGCTTGCAGAGCTGGGTTTATTATGTTGGTAAACAGTGATGATG 198
QY 102 AAGTCTTTCTACTGTGGAGGGGCTAACTGATTTGAGAGCCAGTGAAGACCCCTTGGGA 161
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 199 CAAATGCTTTGCTGTGATGGTGGAGCTCAGGTGTTGGGAATCTGGAGATGCCATGGGT 258
QY 162 ACAACATGCTAAATGTTATCCAGGGTGCAAAATATCTG 198
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Db 259 TCAACATGCCAAGTGGTTTCCAGGTGTCAGTACTTG 295

RESULT 15

AW846425
LOCUS AW846425 532 bp mRNA linear EST 19-MAY-2000
DEFINITION QV0-CT0179-070300-143-d09 CT0179 Homo sapiens cDNA, mRNA sequence.
ACCESSION AW846425
VERSION AW846425.1 GI:7941942
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 532)
Dias Neto,E., Garcia Correia,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Balg,G.S., Simpson,D.H.,
Brunstein,A., deoliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

JOURNAL

MEDLINE

COMMENT

Contact: Simpson A.J.G.
Laboratory of Cancer Genetics

Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?tl=QV0&t2=QV0-CT0179-070
300-143-d09&t3=2000-03-07&t4=1)
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High quality sequence stop: 531.

FEATURES
source

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/dev_stage="Adult"
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Sma1; A mini-library was made by cloning products derived
from ORESTES PCR (U.S. Letters Patent application No. 196
,716 - Ludwig Institute for Cancer Research) profiles
into the pUC 18 vector. Reverse transcription of tissue
mRNA and cDNA amplification were performed under low
stringency conditions."

BASE COUNT 160 a 107 c 122 g 143 t

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Best Local Similarity 68.8%; Pred. No. 4.8e-15;
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||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 96 AGTTAATCTCGAGCAGCTTGCAGAGCTGGGTTTATTATGTTGGTAAACAGTGATGATG 155
QY 102 AAGTCTTTCTACTGTGGAGGGGCTAACTGATTTGAGAGCCAGTGAAGACCCCTTGGGA 161
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 156 CAAATGCTTTGCTGTGATGGTGGAGCTCAGGTGTTGGGAATCTGGAGATGCCATGGGT 215
QY 162 ACAACATGCTAAATGTTATCCAGGGTGCAAAATATCTG 198
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Db 216 TCAACATGCCAAGTGGTTTCCAGGTGTGAGTACTTG 252

Search completed: April 16, 2003, 00:54:57
Job time : 950.375 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:40:42 ; Search time 1031.86 seconds
(without alignments)
5753.635 Million cell updates/sec

Title: US-09-654-743-49
Perfect score: 204
Sequence: 1 gagttaataagattaaaac.....ccccaaattgcagattttac 204

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

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- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
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- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
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- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
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- 28: em.un.*
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- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pln.*
- 35: em.htg_rod.*
- 36: em.htg_mam.*
- 37: em.htg_vrt.*
- 38: em.sy.*
- 39: em.htgo_hum.*
- 40: em.htgo_mus.*
- 41: em.htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	2100	6	AX412124 Sequence
2	204	100.0	2691	6	AR106400 Sequence
3	204	100.0	2891	6	AR116702 Sequence
4	204	100.0	2891	10	MM088990 Mus musculu
5	202.4	99.2	1988	10	MMU36842 Mus musculu
6	189.6	92.9	2032	10	AF304333 Rattus no
7	189.6	92.9	2468	10	AB033366 Rattus no
8	189.6	92.9	3032	10	AF304334 Rattus no
9	188	92.2	1491	10	AF183429 Rattus no
10	172	84.3	1659	6	E31042 Method for
11	172	84.3	1659	9	U32974 Human RAP-1
12	172	84.3	2086	9	BC03729 Homo sapi
13	172	84.3	2404	6	AX429575 Sequence
14	172	84.3	2540	6	AR103281 Sequence
15	172	84.3	2540	6	AX412118 Sequence
16	172	84.3	2540	9	HSU45880 Human X-lin
17	172	84.3	3000	6	AX412131 Sequence
18	172	84.3	5232	6	AR106397 Sequence
19	172	84.3	5232	6	AR116699 Sequence
20	172	84.3	13391	9	HSU331561 Human DNA
21	172	84.3	201197	2	HS424J12 Homo sapien
22	134.4	65.9	187568	9	AP002967 Homo sapi
23	127.8	62.6	7990	6	AX281265 Sequence
24	127.8	62.6	7990	6	AX345060 Sequence
25	110.2	54.0	7990	6	AX381266 Sequence
26	110.2	54.0	7990	6	AX345061 Sequence
27	100.6	49.3	179491	2	AC020673 Homo sapi
28	98.6	48.3	1740	5	AF451854 Gallus ga
29	68	33.3	163882	2	AL627325 Danio rer
30	68	33.3	1346	5	AF442500 Danio rer
31	67	32.8	3264	5	AF008592 Gallus ga
32	67	32.8	9860	5	AF311289 Gallus ga
33	63.8	31.3	2867	5	GGU7486 Gallus gall
34	60.6	29.7	2416	6	AX412128 Sequence
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36	60.6	29.7	2862	6	AR129834 Sequence
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42	59	28.9	2531	9	HUMSCPA Homo sapien
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ALIGNMENTS

RESULT 1	AX412124	Sequence 224 from Patent WO0226968.	2100 bp	DNA	linear	PAT 15-JUN-2002
LOCUS	AX412124	Sequence 224 from Patent WO0226968.				
DEFINITION	AX412124					
ACCESSION	AX412124					
VERSION	AX412124.1	GI:21444584				
KEYWORDS						
SOURCE	house mouse.					
ORGANISM	Mus musculus					
REFERENCE						
AUTHORS	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;					
TITLE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
JOURNAL	Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.					
	Antisense flap nucleic acids and uses thereof					
	Patent: WO 0226968-A 224 04-APR-2002;					

University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)
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Source
1. 2100
/organism="Mus musculus"
/db_xref="taxon:10090"
BASE COUNT 615 a 417 c 482 g 586 t
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 4.3e-61;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGTTTAAATAGATTAATAAACAATTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
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Db 202 GAGTTTAAATAGATTAATAAACAATTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 261
QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120
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Db 262 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 321
QY 121 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
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Db 322 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 381
QY 181 ATATCCCAAAATTCAGATTATC 204
|||||
Db 382 ATATCCCAAAATTCAGATTATC 405
RESULT 2
AR106400 AR106400 2691 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 9 from patent US 6107041.
ACCESSION AR106400
VERSION AR106400.1 GI:12820930
KEYWORDS
Source
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.
TITLE Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease
JOURNAL Patent: US 6107041-A 9 22-AUG-2000;
FEATURES Location/Qualifiers
Source
1. .2691
BASE COUNT 819 a 479 c 562 g 831 t
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Db 867 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 926
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Db 927 ATATCCCAAAATTCAGATTATC 950
RESULT 3
AR106400 AR106400 2691 bp DNA linear PAT 16-MAY-2001
DEFINITION Sequence 9 from patent US 6133437.
ACCESSION AR106400
VERSION AR106400.1 GI:14097024
KEYWORDS
Source
ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.
TITLE Modulation of IAPs for the treatment of proliferative diseases
JOURNAL Patent: US 6133437-A 9 17-OCT-2000;
FEATURES Location/Qualifiers
Source
1. .2691
BASE COUNT 819 a 479 c 562 g 831 t
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Query Match 100.0%; Score 204; DB 6; Length 2691;
Best Local Similarity 100.0%; Pred. No. 4.5e-61;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGTTTAAATAGATTAATAAACAATTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
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Db 747 GAGTTTAAATAGATTAATAAACAATTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 806
QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120
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Db 807 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 866
QY 121 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
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Db 867 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 926
QY 181 ATATCCCAAAATTCAGATTATC 204
|||||
Db 927 ATATCCCAAAATTCAGATTATC 950
RESULT 4
MMU88990 MMU88990 2691 bp mRNA linear ROD 31-MAY-1997
DEFINITION Mus musculus X-linked inhibitor of apoptosis (miap-3) mRNA, complete cds.
ACCESSION U88990
VERSION U88990.1 GI:2138318
KEYWORDS
Source
ORGANISM
Mus musculus.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2691)
AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.
TITLE Genomic Organization and Primary Characterization of miap-3: The Murine Homologue of Human X-linked IAP
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2691)
AUTHORS Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.
TITLE Direct Submission
JOURNAL Submitted (07-FEB-1997) Molecular Genetics, Children's Hospital of Eastern Ontario, 401 Smyth Rd., Ottawa, Ontario K1H 8L1, Canada
FEATURES Location/Qualifiers
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gene
exon

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BASE COUNT
ORIGIN
Query Match 100.0%; Score 204; DB 10; Length 2691;
Best Local Similarity 100.0%; Pred. No. 4.5e-61;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAAATAGATAAAACATTTGCTAACCTCCCAAGTAGTAGTCTCTGTTTCAGCATCA 60
Db 747 GAGTTTAAATAGATAAAACATTTGCTAACCTCCCAAGTAGTAGTCTCTGTTTCAGCATCA 806

QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGTGCATGTTTCAGT 120
Db 807 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGTGCATGTTTCAGT 866

QY 121 TGTCTATGGCGCAATAGATAGATGCGAGTATGCGAGTCTGTTGGAAGACACAGGAGA 180
Db 867 TGTCTATGGCGCAATAGATAGATGCGAGTATGCGAGTCTGTTGGAAGACACAGGAGA 926

QY 181 ATATCCCCAAATTCAGATTATC 204
Db 927 ATATCCCCAAATTCAGATTATC 950

RESULT 5
MMU36842
LOCUS
DEFINITION
Mus musculus IAP homolog A (MIHA) mRNA, complete cds.
ACCESSION
U36842.1
VERSION
U36842.1
KEYWORDS
1988 bp mRNA linear ROD 05-JUN-1996
SOURCE
house mouse strain=C57 Black 6 x CBA.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 1988)
Uren.A.G., Pakusch.M., Hawkins.C.J., Puls.K.L. and Vaux.D.L.
Cloning and expression of apoptosis inhibitory protein homologs
that function to inhibit apoptosis and/or bind tumor necrosis
factor receptor-associated factors

```

```

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (10), 4974-4978 (1996)
MEDLINE 96209843
PUBMED 8643514
REFERENCE 2 (bases 1 to 1988)
AUTHORS Vaux,D.L., Uren,A.G. and Pakusch,M.
TITLE Direct Submission
JOURNAL Submitted (21-SEP-1995) M. Pakusch, The Walter and Eliza Hall
Institute, Royal Parade, Parkville, Victoria 3050, Australia
FEATURES
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212..1702
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/feature="apoptosis inhibitor; homolog of Baculovirus IAP
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CSEEARLKSFQWNPYAHLPRELASAGLYTGADQVQCFCCGKLEWPCDRAMS
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QYVINNIHTHLESLGRTAETPLTKKIDDTIFQNPVQEAIRMGFSFKDIKTM
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BASE COUNT
ORIGIN
Query Match 99.2%; Score 202.4; DB 10; Length 1988;
Best Local Similarity 99.5%; Pred. No. 1.16e-60;
Matches 203; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGTGCATGTTTCAGT 120
Db 347 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGTGCATGTTTCAGT 406

QY 121 TGTCTATGGCGCAATAGATAGATGCGAGTATGCGAGTCTGTTGGAAGACACAGGAGA 180
Db 407 TGTCTATGGCGCAATAGATAGATGCGAGTATGCGAGTCTGTTGGAAGACACAGGAGA 466

QY 181 ATATCCCCAAATTCAGATTATC 204
Db 467 ATATCCCCAAATTCAGATTATC 490

RESULT 6
AF304333

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LOCUS
DEFINITION AF304333 2032 bp mRNA linear ROD 19-DEC-2000
 complete cds.
ACCESSION AF304333
VERSION AF304333.1 GI:11890718
SOURCE Rattus norvegicus.
ORGANISM Rattus norvegicus.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
REFERENCE 1 (bases 1 to 2032)
AUTHORS Lareu, R.R., Bradley, C.K., Lacher, M., Friis, R.R. and
 Dharmarajan, A.M.
TITLE Cloning, characterization and regulation of an inhibitor of
 apoptosis protein in the rat corpus luteum
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2032)
AUTHORS Lareu, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Anatomy and Human Biology, University of
 Western Australia, Verdum St, Nedlands, WA 6907, Australia
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 CSEARLKTQWNPDIYAHLSPRELASAGLYTGIDQVQCFCCGKLNWPCDRAMS
 EHRHFFNCFVFLGRNVNVRSESGVSSDRNPNSTNSPRNPAEYDARIYVFTGLY
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 BASE COUNT 609 a 385 c 473 g 565 t
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 Best Local Similarity 95.6%; Pred. No. 5.7e-56;
 Matches 195; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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 Db 200 GAGTTTAATAGATTAAACATTTGCTTACTCCCAAGTAGTAGTCTCTGTTTCAGCATCA 259
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 QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAGGACACCGCTGCAATCTTCAGT 120
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 Db 260 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAGGACACCGCTGCAATCTTCAGT 319
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 QY 121 TGTATCGCGCAATAGATAGATAGATGCGAGCTATGAGACTTCAGCTGTGGAAGACACAGAGA 180
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 QY 181 ATATCCCAAAATTCGAGATTATC 204
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 Db 380 ATATCCCAAAATTCGAGATTATC 403
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RESULT 7
AB033366
LOCUS AF304334 2468 bp mRNA linear ROD 15-OCT-1999
DEFINITION Rattus norvegicus riap3 mRNA, complete cds.
 complete cds.
ACCESSION AF304334
VERSION AF304334.1 GI:11890720
KEYWORDS Rattus norvegicus.
SOURCE

ACCESSION AB033366
VERSION AB033366.1 GI:6045147
KEYWORDS RIAP3.
SOURCE Rattus norvegicus cDNA to mRNA.
ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
 Rattus.
REFERENCE 1 (bases 1 to 2468)
AUTHORS Saito, N.
TITLE Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA
JOURNAL Published Only in DataBase (1999)
REFERENCE 2 (bases 1 to 2468)
AUTHORS Saito, N.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1999) Nobuhito Saito, University of Tokyo,
 Department of Neurosurgery; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655,
 Japan [E-mail:n.saito-tyk@umin.ac.jp, Tel:+81-3-5800-8853,
 Fax:+81-3-5800-8655]
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 BASE COUNT 690 a 481 c 609 g 588 t
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 Query Match 92.9%; Score 189.6; DB 10; Length 2468;
 Best Local Similarity 95.6%; Pred. No. 5.9e-56;
 Matches 195; Conservative 0; Mismatches 9; Indels 0; Gaps 0;
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 QY 181 ATATCCCAAAATTCGAGATTATC 204
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 Db 585 ATATCCCAAAATTCGAGATTATC 608
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RESULT 8
AF304334
LOCUS AF304334 3032 bp mRNA linear ROD 19-DEC-2000
DEFINITION Rattus norvegicus clone 2 inhibitor of apoptosis protein 3 mRNA,
 complete cds.
ACCESSION AF304334
VERSION AF304334.1 GI:11890720
KEYWORDS Rattus norvegicus.
SOURCE

ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 3032)
AUTHORS Lareu, R.R., Bradley, C.K., Lacher, M., Friis, R.R. and Dharmarajan, A.M.
TITLE Cloning, characterization and regulation of an inhibitor of apoptosis protein in the rat corpus luteum
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 3032)
AUTHORS Lareu, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Anatomy and Human Biology, University of Western Australia, Verdum St, Nedlands, WA 6907, Australia

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Location/Qualifiers
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Best Local Similarity 95.6%; Pred. No. 61e-56;
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QY 181 ATATCCCAAAATTCAGATTATC 204
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RESULT 9
AF183429
LOCUS Rattus norvegicus inhibitor of apoptosis protein 3 mRNA, complete cds.
DEFINITION AF183429
ACCESSION AF183429
VERSION AF183429.1 GI:10765280
KEYWORDS Norway rat.
SOURCE Rattus norvegicus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 1491)
AUTHORS Holcik, M., Lefebvre, C.A., Hicks, K. and Korneluk, R.G.
TITLE Cloning and characterization of the rat homologues of the Inhibitor of Apoptosis protein 1, 2, and 3 genes
JOURNAL BMC Genomics 3 (1), 5 (2002)
PUBMED 11860601
REFERENCE 2 (bases 1 to 1491)
AUTHORS Holcik, M., Lefebvre, C.A., Hicks, K. and Korneluk, R.G.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-1999) Department of Biochemistry, Microbiology and Immunology, University of Ottawa, 451 Smyth Road, Ottawa, Ontario K1H 8M5, Canada

FEATURES
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/db_xref="taxon:10116"
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BASE COUNT 464 a 282 c 357 g 388 t
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Best Local Similarity 95.1%; Pred. No. 2e-55;
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QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
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QY 61 ACATTGGCGGAGCTGGTTCCTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120
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QY 121 TGTCTATGCGCAATAGATAGATGCGAGTATGAGACTCAGCTGTTGGAAGACACAGGAGA 180
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QY 181 ATATCCCAAAATTCAGATTATC 204
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Db 256 ATATCCCAAAATTCAGATTATC 279
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RESULT 10
E31042
LOCUS Method for screening substance inhibiting binding to XIAP.
DEFINITION E31042
ACCESSION E31042
VERSION E31042.1 GI:13017307
KEYWORDS JP 1999326328-A/2.
SOURCE unidentified.
ORGANISM unclassified.
REFERENCE 1 (bases 1 to 1659)
AUTHORS Kunihiro, M.
TITLE Method for screening substance inhibiting binding to XIAP
JOURNAL Patent: JP 1999326328-A 2 26-NOV-1999;
KUNIHIRO MATSUMOTO
COMMENT OS Unidentified

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PN JP 1999326328-A/2
PD 26-NOV-1999
PF 13-MAY-1998 JP 1998130378
PR KUNIHITO MATSUMOTO
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PC A61K39/395,
PC A61K45/00, A61K45/00, A61K45/00, C07K7/06, C07K14/47, PC
GOIN33/536,
PC GOIN33/536, GOIN33/536, C12N15/09, C12P21/08, A61K37/02,
A61K37/02, PC A61K37/02,
PC A61K37/02, A61K37/24, C12N15/00
CC Strandedness: Double;
CC Topology: Linear;
FH Key Location/Qualifiers
FT CDS 82..1572.
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Best Local Similarity 90.2%; Pred. No. 1e-49;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY 1 GAGTTAATAGATTAAACATTTGCTAATCTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
DB 157 GAGTTAATAGATTAAACATTTGCTAATCTCCCAAGTAGTAGTCTGTTTCAGCATCA 216
QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120
DB 217 ACATGGCAGCAGCAGGGTTCTTTATCTGTTGAGGAGATACCGTGGGTCCTTAGT 276
QY 121 TGTCATGGCGCAATAGATAGATGCGAGTATGGAGACTGCTGTTGGAAGACACAGGAGA 180
DB 277 TGTCATGCGAGCTGTAGATAGATGCGCAATATGGAGACTGCGAGCTTGGAGACACAGGAAA 336
QY 181 ATATCCCAAAATTCAGATTATC 204
DB 337 GTATCCCAAAATTCAGATTATC 360

RESULT 11
HSU32974
LOCUS      1659 bp mRNA linear PRI 12-JUN-1996
DEFINITION Human IAP-like protein ILP mRNA, complete cds.
ACCESSION  U32974
VERSION     U32974.1 GI:1016687
KEYWORDS    apoptosis; ring finger; zinc finger.
SOURCE      Homo sapiens.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 1659)
AUTHORS     Duckett,C.S., Nava,V.E., Gedrich,R.W., Clem,R.J., Van Dongen,J.L.,
            Gilfillan,M.C., Shiels,H., Hardwick,J.M., and Thompson,C.B.
TITLE       A conserved family of cellular genes related to the baculovirus iap
            gene and encoding apoptosis inhibitors
JOURNAL     EMBO J. 15 (11), 2685-2694 (1996)
MEDLINE     96256286
PUBMED      8654366
REFERENCE   2 (bases 1 to 1659)
AUTHORS     Duckett,C.S. and Thompson,C.B.
TITLE       Direct Submission
JOURNAL     Submitted (01-AUG-1995) Colin Duckett, Howard Hughes Medical
            Institute, The University of Chicago, 924 East 57th Street,
            Chicago, IL 60637, USA
FEATURES             Location/Qualifiers
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          /db_xref="taxon:9606"

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CDS

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BASE COUNT      519 a 296 c 385 g 459 t
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Best Local Similarity 90.2%; Pred. No. 1e-49;
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QY 1 GAGTTAATAGATTAAACATTTGCTAATCTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
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DB 217 ACATGGCAGCAGCAGGGTTCTTTATCTGTTGAGGAGATACCGTGGGTCCTTAGT 276
QY 121 TGTCATGGCGCAATAGATAGATGCGAGTATGGAGACTGCTGTTGGAAGACACAGGAGA 180
DB 277 TGTCATGCGAGCTGTAGATAGATGCGCAATATGGAGACTGCGAGCTTGGAGACACAGGAAA 336
QY 181 ATATCCCAAAATTCAGATTATC 204
DB 337 GTATCCCAAAATTCAGATTATC 360

RESULT 12
BC032729
LOCUS      2086 bp mRNA linear PRI 27-JUN-2002
DEFINITION Homo sapiens, baculoviral IAP repeat-containing 4, clone MGC:45369
            IMAGE:5532247, mRNA, complete cds.
ACCESSION  BC032729
VERSION     BC032729.1 GI:21619763
KEYWORDS    MGC.
SOURCE      human.
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 2086)
AUTHORS     Strausberg,R.
TITLE       Direct Submission
JOURNAL     Submitted (06-JUN-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
            NIH-MGC Project URL: http://mgc.nci.nih.gov
            Contact: MGC help desk
            Email: cgabbs-r@mail.nih.gov
            Tissue Procurement: ATCC

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CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: National Institutes of Health Intramural
 Sequencing Center (NISC),
 Gaithersburg, Maryland;
 Web site: <http://www.nisc.nih.gov/>
 Contact: nisc.mc@nih.gov
 Akhter, N., Ayele, K., Beckstrom-Sternberg, S.M., Benjamin, B.,
 Blakesley, R.W., Bouffard, G.G., Green, K., Brinkley, C., Brooks, S.,
 Dietrich, N.L., Granite, S., Guan, X., Gupta, J., Haghighi, P.,
 Hansen, N., Ho, S.-L., Karlins, E., Kwong, P., Laric, P., Legaspi, R.,
 Maduro, Q.L., Masello, C., Maskeri, B., Mastrian, S.D., McCloskey, J.C.,
 McDowell, J., Pearson, R., Stantripop, S., Thomas, P.J., Touchman, J.W.,
 Young, A.C., Vogt, J.L., Walker, M.A., Wetherby, K.D., Wiggins, L.,
 Young, A., Zhang, L.-H. and Green, E.D.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAC Plate: 69 Row: j Column: 18
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4502142.

FEATURES
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 /protein_id="AAH32729.1"
 /db_xref="GI:21619764"
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 YSVNQLARAGYALGEGKVKCFHCGGLTDWKPSEDEQHWKWPCKYLLLEOK
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Query Match 84.3%; Score 172; DB 9; Length 2086;
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 Qy 1 GAGTTTAATAGATTAATAAACAATTTGCTAACCTCCCAAGTAGTAGTCCTGTTTCAGCATCA 60
 Db 154 GAGTTTAATAGATTAATAAACAATTTGCTAACCTCCCAAGTAGTAGTCCTGTTTCAGCATCA 213
 Qy 61 ACATTGGCGGAGCTGGTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120
 Db 214 ACATTGGCGGAGCTGGTCTTTATACCGGTGAAGGAGATACCGTGCCTGCTTTAGT 273
 Qy 121 TGTCATCGGCAANTAGATAGATGCGAGTATGAGACTAGCTGTTGGAAGACACAGGAGA 180
 Db 274 TGTCATCGCTAGATAGATAGATGCGAGTATGAGACTAGCTGTTGGAAGACACAGGAGA 333
 Qy 181 ATATCCCCAAATTCGAGATTTATC 204
 Db 334 GTATCCCCAAATTCGAGATTTATC 357
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 AX429575 2404 bp DNA linear PAT 21-JUN-2002
 LOCUS Sequence 38 from Patent WO0226820.

ACCESSION AX429575
 VERSION AX429575.1 GI:21540833
 KEYWORDS human.
 SOURCE Homo sapiens
 ORGANISM human.
 REFERENCE 1
 AUTHORS Cohen, D., Dengler, U.J., Finelli, A.L., Freuler, F., Konsolaki, M.,
 Reinhardt, M.W. and Zeman, S.
 TITLE Transgenic drosophila melanogaster expressing beta amyloid
 JOURNAL Patent: WO 0226820-A 38 04-APR-2002;
 NOVARTIS ERIND VERWALT GMBH (AT)
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 /db_xref="taxon:9606"
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 Db 109 GAGTTTAATAGATTAATAAACAATTTGCTAACCTCCCAAGTAGTAGTCCTGTTTCAGCATCA 168
 Qy 61 ACATTGGCGGAGCTGGTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120
 Db 169 ACATTGGCGGAGCTGGTCTTTATACCGGTGAAGGAGATACCGTGCCTGCTTTAGT 228
 Qy 121 TGTCATCGGCAANTAGATAGATGCGAGTATGAGACTAGCTGTTGGAAGACACAGGAGA 180
 Db 229 TGTCATCGCTAGATAGATAGATGCGAGTATGAGACTAGCTGTTGGAAGACACAGGAGA 288
 Qy 181 ATATCCCCAAATTCGAGATTTATC 204
 Db 289 GTATCCCCAAATTCGAGATTTATC 312
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 AX429575 2540 bp DNA linear PAT 14-FEB-2001
 LOCUS Sequence 1 from patent US 6087173.
 DEFINITION Antisense modulation of X-linked inhibitor of apoptosis expression
 ACCESSION AR103281
 VERSION AR103281.1 GI:12814869
 KEYWORDS Unknown.
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 2540)
 AUTHORS Bennett, C.Frank., Ackermann, E.J. and Cowsert, L.M.
 TITLE Antisense modulation of X-linked inhibitor of apoptosis expression
 JOURNAL Patent: US 6087173-A 1 11-JUL-2000;
 FEATURES Location/Qualifiers
 source 1..2540
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 BASE COUNT 781 a 415 c 571 g 773 t
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 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 Qy 1 GAGTTTAATAGATTAATAAACAATTTGCTAACCTCCCAAGTAGTAGTCCTGTTTCAGCATCA 60
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 Db 169 ACATTGGCGGAGCTGGTCTTTATACCGGTGAAGGAGATACCGTGCCTGCTTTAGT 228

Search completed: April 15, 2003, 23:25:25
Job time : 1035.86 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:38:17 ; Search time 136.354 seconds
(without alignments)
3369,223 Million cell updates/sec

Title: US-09-654-743-49
Perfect score: 204
Sequence: 1 gatttaaatagattaaac.....ccccaaattgcagatttacc 204

Scoring table: IDENTITY_NUC
Gapop 10.0, Capext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	2100	18	Mouse apoptosis in
2	204	100.0	2100	24	Mouse cDNA encoding
3	204	100.0	2691	19	Murine XIAP coding
4	202.4	99.2	1988	18	Mouse inhibitor of
5	172	84.3	1659	21	Human XIAP coding
6	172	84.3	2404	24	DNA of APP related
7	172	84.3	2540	18	Human apoptosis in
8	172	84.3	2540	21	Human X-linked inh
9	172	84.3	2540	24	Human cDNA encoding

SUMMARIES

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

10	172	84.3	3000	24	ABK93875
11	172	84.3	5232	19	AAV55038
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13	127.8	62.6	7990	24	ABL54308
14	110.2	54.0	7990	24	ABL32158
15	110.2	54.0	7990	24	ABL32159
16	60.6	29.7	2416	18	AAV70841
17	60.6	29.7	2416	24	ABK93874
18	60.6	29.7	2862	18	AAV61592
19	60.6	29.7	3151	19	AAV55043
20	59	28.9	649	24	ABQ60576
21	59	28.9	2580	18	AAV70838
22	59	28.9	2580	24	ABK93871
23	59	28.9	2589	18	AAV61590
24	59	28.9	3532	18	AAV72711
25	59	28.9	3532	20	AAZ22143
26	59	28.9	3532	24	ABN96857
27	59	28.9	3732	19	AAV55040
28	57.4	28.1	2291	22	AAV506025
29	55.8	27.4	2474	18	AAV70840
30	55.8	27.4	2474	24	ABK93873
31	55.8	27.4	2676	19	AAV55042
32	54.4	26.7	2666	18	AAV70837
33	54.4	26.7	2676	24	ABK93870
34	54.4	26.7	3076	18	AAV72712
35	54.4	26.7	3076	20	AAZ41005
36	54.4	26.7	3076	20	AAZ22096
37	54.4	26.7	3076	24	ABL62746
38	54.4	26.7	3076	24	ABL66325
39	54.4	26.7	6669	19	AAV55039
40	54.4	26.7	6669	24	ABK93875
41	54.2	26.6	1559	24	ABK13197
42	54.2	26.6	1758	24	ABK14677
43	54.2	26.6	1758	24	ABK14678
44	54.2	26.6	4993	22	AAO30581
45	52.8	25.9	794	24	ABL55635

ALIGNMENTS

RESULT 1
AAV70839
ID AAT70839 standard; cDNA; 2100 BP.
XX AAT70839;
AC AAT70839;
XX 02-SEP-1997 (first entry)
DT
DE Mouse apoptosis inhibitor m-xiap cDNA.

KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
KW M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;
KW ischaemia; myocardial infarction; stroke;
KW reperfusion injury; toxin-induced liver disease; gene therapy;
diagnosis; ds.
XX Mus sp.
XX
FH Key Location/Qualifiers
FT CDS 127..1617
ET /*tag= a

XX W09706255-A2.
XX 20-FEB-1997.
XX 05-AUG-1996; 96WO-IB01022.
XX 22-DEC-1995; 95US-0576956.
XX 04-AUG-1995; 95US-0511485.
XX (UYOT-) UNIV OTTAWA.

Human cDNA encoding
Human XIAP coding
Chemically treated
Human immune syste
Chemically treated
Human immune syste
Mouse apoptosis in
Mouse cDNA encoding
Murine c-IAP. Mus
Human HIAP-2 codi
Human colon cancer
Human apoptosis in
Human cDNA encoding
Human c-IAP1. Hom
Human inhibitor of
Human cellular inh
Gene #3355 used to
Human HIAP-2 codin
Angiotensin conver
Mouse apoptosis in
Mouse cDNA encoding
Murine HIAP-1 codi
Human apoptosis in
Human cDNA encoding
Human inhibitor of
Human cellular inh
Human cellular inh
Breast cancer rela
Lung cancer relate
Human HIAP-1 codin
Human cDNA encoding
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Human inhibitor of
Human IAP-like pro
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XX PI Baird S, Korneluk RG, Liston P, Mackenzie AE;
 XX DR WPI: 1997-154262/14.
 XX DR P-PSDB: AAW19584.
 XX
 PT Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
 PT of susceptibility to apoptotic disease
 XX
 PS Claim 11; Page 78-79; 219pp; English.
 XX
 CC Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and
 CC hiap-2 genes (AA70836-41) respectively code for a new class of
 CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis
 CC (IAP). The murine xiap gene (for X-linked IAP gene) sequence was
 CC constructed from 12 overlapping clones isolated from a mouse
 CC embryo lambda-gt10 cDNA library and from a mouse FIX II genomic
 CC library using human xiap cDNA as probe. IAP nucleic acids can be
 CC used to express IAP polypeptides in cells and animals to inhibit
 CC apoptosis, and as primers and probes to identify and isolate
 CC additional IAP genes, as well as in methods for treating diseases
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).
 XX
 SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;
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 Best Local Similarity 100.0%; Pred. No. 2.4e-61;
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 QY 181 ATATCCCAAAATTCAGATTATC 204
 Db 382 ATATCCCAAAATTCAGATTATC 405
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 ABK93872
 ID ABK93872 standard; cdna; 2100 BP.
 XX AC ABK93872;
 XX
 DT 26-AUG-2002 (first entry)
 DE Mouse cDNA encoding inhibitor of apoptosis, XIAP.
 XX
 KW Mouse; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Mus sp.
 XX
 XX WO200226968-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-CA01379.
 XX
 XX 28-SEP-2000; 2000US-0672717.
 PR

XX PA (UYOT-) UNIV OTTAWA.
 XX PI (AEGE-) AEGERA THERAPEUTICS INC.
 XX DR Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX WPI: 2002-479562/51.
 XX DR P-PSDB: ABG65666.
 XX
 PT Novel antisense inhibitor of apoptosis nucleic acid useful for
 PT enhancing apoptosis in a cell, for treating cancer and other
 PT proliferative diseases
 XX
 PS Disclosure; Fig 4; 135pp; English.
 XX
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (1) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
 CC cDNA sequence.
 XX
 SQ Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;
 Query Match 100.0%; Score 204; DB 24; Length 2100;
 Best Local Similarity 100.0%; Pred. No. 2.4e-61;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGGTGCAATGTTTCAGT 120
 Db 262 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGGTGCAATGTTTCAGT 321
 QY 121 TGTCTATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
 Db 322 TGTCTATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 381
 QY 181 ATATCCCAAAATTCAGATTATC 204
 Db 382 ATATCCCAAAATTCAGATTATC 405
 RESULT 3
 AAV55041
 ID AAV55041 standard; cdna; 2691 BP.
 XX AAV55041;
 AC AAV55041;
 XX
 DT 13-NOV-1998 (first entry)
 DE Murine XIAP coding sequence.
 XX
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.
 XX
 OS Mus sp.
 XX
 XX Key Location/Qualifiers
 FH

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FT /product= XIAP
XX
XX WO9835693-A2.
XX
XX 20-AUG-1998.
XX
XX 13-FEB-1998; 98WO-IB00781.
XX
XX 13-FEB-1997; 97US-0800929.
XX
XX (UYOT- } UNIV OTTAWA.
XX
XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
XX Tsang B;
XX
XX WPI: 1998-467164/40.
XX P-PSDB; AAW69297.
XX
XX Inducing apoptosis in proliferative mammalian cells with inhibitor
XX of IAP or NAIP polypeptide - also methods for prognosis based on
XX presence of IAP and NAIP, specifically applied to cancers involving
XX p53 mutations
XX
XX Claim 13; Fig 4; 147pp; English.
XX
XX This sequence encodes the mouse XIAP protein, which is a inhibitor of
XX apoptosis protein (IAP), and can be used in the method of the invention.
XX The method is for enhancing apoptosis in cells from a mammal with
XX proliferative disease by treatment with a compound that inhibits
XX biological activity of an IAP or NAIP polypeptide. The inhibitory
XX compounds are used to treat proliferative diseases, specially cancers of
XX ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
XX liver, nasopharynx, thyroid, central nervous system, prostate, colon,
XX rectum, cervix or endometrium, particularly to increase their sensitivity
XX to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
XX detected in many cancers and are associated with poor prognosis,
XX resistance to chemotherapeutic agents and mutations in p53 (it is
XX suggested that wild-type p53 suppresses transcription of the IAP or NAIP
XX genes). Transgenic animals are used for testing the effects of antisense
XX oligonucleotides and for screening for the inhibitors.
XX
XX Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 other;
XX
XX Query Match 100.0%; Score 204; DB 19; Length 2691;
XX Best Local Similarity 100.0%; Pred. No. 2.7e-61;
XX Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
XX |
XX DB 747 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 806
XX |
XX QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120
XX |
XX DB 807 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 866
XX |
XX QY 121 TGTCAATGCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
XX |
XX DB 867 TGTCAATGCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 926
XX |
XX QY 181 ATATCCCAAAATGCGAGATTATC 204
XX |
XX DB 927 ATATCCCAAAATGCGAGATTATC 950
XX |
XX
XX RESULT 4
XX AAT72710
XX ID AAT72710 standard; DNA: 1988 BP.
XX AC AAT72710;
XX
XX DT 16-SEP-1997 (first entry)

```

```

XX Mouse inhibitor of apoptosis protein homologue MIHA DNA.
XX
XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
XX degenerative disease; infectious disease; autoimmune disease;
XX cancer; gene therapy; diagnosis; ss.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX CDS 212..1702
XX /*tag= a
XX
XX WO9723501-A1.
XX
XX 03-JUL-1997..
XX
XX 20-DEC-1996; 96WO-AU00827.
XX
XX 22-DEC-1995; 95AU-0007275.
XX
XX (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX Vaux DL;
XX
XX WPI: 1997-350966/32.
XX P-PSDB; AAW19745.
XX
XX Isolated protein homologues of viral inhibitors of apoptosis - used
XX to modulate apoptosis for treatment of degenerative, infectious or
XX autoimmune diseases and cancer
XX
XX Claim 24; Page 44-47; 136pp; English.
XX
XX An isolated nucleic acid molecule (AAT72710) codes for mammalian IAP
XX homologue A (MIHA) (AAW19745), a murine homologue of baculovirus
XX inhibitor of apoptosis protein (IAP). It was isolated from a mouse
XX liver cDNA library on the basis of homology to Orgyia pseudotsuguta
XX polyhedrosis virus IAP BIR and RING finger amino acid motifs.
XX Animal IAP homologue nucleic acids (see also AAT72711-17) can be used
XX to produce polypeptides useful in methods for modulating apoptosis
XX in animal cells, specifically for treatment, by inhibition, of
XX degenerative and infectious disease or, by promotion, of cancer and
XX autoimmune disease, and can be used for gene therapy of these
XX diseases.
XX
XX Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 other;
XX
XX Query Match 99.2%; Score 202.4; DB 18; Length 1988;
XX Best Local Similarity 99.5%; Pred. No. 8.5e-61;
XX Matches 203; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
XX |
XX DB 287 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 346
XX |
XX QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120
XX |
XX DB 347 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 406
XX |
XX QY 121 TGTCAATGCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
XX |
XX DB 407 TGTCAATGCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 466
XX |
XX QY 181 ATATCCCAAAATGCGAGATTATC 204
XX |
XX DB 467 ATATCCCAAAATGCGAGATTATC 490
XX |
XX
XX RESULT 5
XX AA248862
XX ID AA248862 standard; cDNA: 1659 BP.
XX
XX

```


AC AAZ48862;
 XX
 DT 24-MAR-2000 (first entry)
 XX
 DE Human XIAP coding sequence.
 XX
 KW Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
 KW transforming growth factor-beta activated kinase 1; monocyte migration;
 KW TAK1 binding protein 1; extracellular matrix protein production;
 KW cell growth inhibitor; beta-amyloid protein deposition;
 KW immunosuppression; Transforming growth factor-beta; ds.
 OS
 XX Homo sapiens.
 XX
 FH JP11326328-A.
 PN
 XX
 PD 26-NOV-1999.
 XX
 XX 13-MAY-1998; 98JP-0130378.
 XX
 XX 13-MAY-1998; 98JP-0130378.
 XX
 PA (MATS/) MATSUMOTO K.
 XX
 DR WPI; 2000-078337/07.
 DR P-PSDB; AAY59451.
 XX
 PT Screening a substance which inhibits combination of the X-linked
 PT inhibitor of apoptosis protein
 XX
 XX Disclosure; Page 28-30; 43pp; Japanese.
 XX
 CC This sequence encodes the human XIAP protein.
 CC The invention relates to a method for screening a substance inhibiting
 CC the formation of a complex between XIAP and TAB1, in which X-linked
 CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta
 CC activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be
 CC tested are contacted with each other and then the presence or formation
 CC of a complex between XIAP and TAB1 is detected. The substance can be used
 CC as a drug for extracellular matrix protein production enhancement, cell
 CC growth inhibition, monocyte migration, physiologically active substance
 CC induction, immunosuppression, and beta-amyloid protein deposition. A
 CC substance inhibiting the formation of a complex between TAB1 and XIAP as
 CC well as between XIAP and TGF-beta (Transforming growth factor-beta) type
 CC I and/or type II receptor is useful as a drug.
 XX
 SQ Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;
 Query Match 84.3%; Score 172; DB 21; Length 1659;
 Best Local Similarity 90.2%; Pred. No. 4.1e-50;
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 GAGTTTAATAGATTAAACATTTGCTAATCTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
 DB 157 GAGTTTAATAGATTAAACATTTGCTAATCTCCCAAGTAGTAGTCTGTTTCAGCATCA 216
 QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120
 DB 217 ACATGGCGACGACGAGGTTCTTTATACCGGTGAAGGAGATACCGTGCGGTGTTTGT 276
 QY 121 TGTGATCGGCAATAGATAGATGCGATGATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
 DB 277 TGTGATCGCTGTGATAGATAGTGAATATGGAGACTCAGCAGTTGGAAGACACAGGAAA 336
 QY 181 ATATCCCAATTCAGATTTATC 204
 DB 337 GTATCCCAATTCAGATTTATC 360
 RESULT 6
 AAK99405
 ID AAK99405 standard; DNA; 2404 BP.
 XX

AC AAK99405;
 XX
 DT 27-JUN-2002 (first entry)
 XX
 DE DNA of APP related human homologue hcp35211.
 XX
 KW Neuroprotective; nootropic; transgenic fly; Alzheimer's disease; Abeta;
 KW amyloid precursor protein; tissue-specific expression control; human APP;
 KW APP pathway modulator; gene therapy; gene; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FH CDS 692..1528
 FT /*tag= a
 FT /product= "Protein of human homologue hcp35211"
 FT /note= "No start codon"
 XX
 XX WO200226820-A2.
 XX
 XX 04-APR-2002.
 XX
 XX 01-OCT-2001; 2001WO-EP11345.
 XX
 XX 29-SEP-2000; 2000US-236893P.
 XX
 XX 14-JUN-2001; 2001US-298309P.
 XX
 XX (NOVS) NOVARTIS AG.
 XX (NOVS) NOVARTIS-ERFINDUNGEN VERN GES MBH.
 XX
 XX Cohen D, Dengler UJ, Finelli AL, Freuler F, Konsolaki M;
 XX Reinhardt MWM, Zusman S;
 PI
 XX
 XX WPI; 2002-315796/35.
 XX P-PSDB; AAO20511.
 DR
 XX
 PT New transgenic fly, containing DNA encoding an Abeta portion of human
 PT APP, useful for identifying agents which modulate the APP pathway and
 PT which can be used to treat Alzheimer's disease.
 XX
 XX Example 4; Page 111; 129pp; English.
 PS
 XX The invention relates to a transgenic fly whose genome comprises DNA
 CC encoding a polypeptide having the Abeta portion of human amyloid
 CC precursor protein (APP), fused to a signal sequence. The DNA sequence
 CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
 CC the specification. The DNA sequence is operably linked to a tissue-
 CC specific expression control sequence. Expression of the sequence gives
 CC the fly an altered phenotype. The purpose of the invention is for
 CC identifying agents that inhibit or promote the expression and/or function
 CC of genes or encoded polypeptides which modify the APP pathway. The agent
 CC is a compound, triple helix DNA, antisense oligonucleotide, double
 CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
 CC to treat conditions such as Alzheimer's disease. The agent can be used as
 CC an APP pathway modulator or in gene therapy. This polynucleotide sequence
 CC represents the DNA of the APP related human homologue hcp35211.
 XX
 SQ Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 other;
 Query Match 84.3%; Score 172; DB 24; Length 2404;
 Best Local Similarity 90.2%; Pred. No. 4.8e-50;
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 GAGTTTAATAGATTAAACATTTGCTAATCTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
 DB 109 GAGTTTAATAGATTAAACATTTGCTAATTTCCCAAGTAGTAGTCTGTTTCAGCATCA 168
 QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120
 DB 169 ACATGGCGACGACGAGGTTCTTTATACCGGTGAAGGAGATACCGTGCGGTGTTTGT 228
 QY 121 TGTGATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
 XX

Db 229 TGTCTATGCTAGATAGTGGCAATATGGAGACTCAGCAGTGGAGACACAGGAAA 288

QY 181 ATATCCCAAAATTCAGATTATC 204
 |||||
 Db 289 GATATCCCAAAATTCAGATTATC 312

RESULT 7
 AAT70836
 ID AAT70836 standard; cDNA; 2540 BP.
 AC AAT70836;
 XX
 DT 02-SEP-1997 (first entry)
 XX
 DE Human apoptosis inhibitor xiap cDNA.
 XX
 KW Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
 KW XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;
 KW ischaemia; myocardial infarction; stroke;
 KW reperfusion injury; toxin-induced liver disease; gene therapy;
 KW diagnosis; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 34..1527
 FT /*tag= a
 XX
 XX W097062255-A2.
 XX
 PD 20-FEB-1997.
 XX
 XX 05-AUG-1996; 96WO-1B01022.
 XX
 XX 22-DEC-1995; 95US-0576956.
 PR 04-AUG-1995; 95US-0511485.
 XX
 XX (UYOT-) UNIV OTTAWA.
 XX
 XX Baird S, Korneluk RG, Liston P, Mackenzie AE;
 DR WPI; 1997-154262/14.
 DR P-PSDB; AAW19581.
 XX
 XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
 PT of susceptibility to apoptotic disease
 XX
 PS Claim 12; Page 67-68; 219pp; English.
 XX
 CC Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and
 CC hiap-2 genes (AAT70836-41) respectively code for a new class of
 CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis
 CC (IAP). The xiap gene (for X-linked IAP gene) was isolated from a
 CC human fetal brain zapII cDNA library using an X-linked sequence
 CC tag site that shows strong homology with the conserved ring zinc
 CC finger domain of baculovirus CpiAP and OptAP genes. The gene was
 CC assigned to chromosome Xq25 by FISH. IAP nucleic acids can be used
 CC to express IAP polypeptides in cells and animals to inhibit
 CC apoptosis, and as primers and probes to identify and isolate
 CC additional IAP genes, as well as in methods for treating diseases
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).
 XX
 XX Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 1 other;
 SQ

Query Match 84.3%; Score 172; DB 18; Length 2540;
 Best Local Similarity 90.2%; Pred. No. 4.9e-50;
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTATAGATTAAACACTTTTGGCTAAATTTCCAGTGGTCTGTTTCAGCATCA 168
 |||||
 Db 109 GAGTTTATAGATTAAACACTTTTGGCTAAATTTCCAGTGGTCTGTTTCAGCATCA 168

QY 61 ACATTGCGGAGCTGGGTTTCTTTATACCGGTGAAGGAGACACCGTCAATGTTTCAGT 120
 |||||
 Db 169 AACTGGCAGCAGCAGGTTCTTTATACCGGTGAAGGAGATACCGTGGCGTGTTCAGT 228
 |||||
 QY 121 TGTCTATGCTAGATAGTGGCAATATGGAGACTCAGCAGTGGAGACACAGGAAA 180
 |||||
 Db 229 TGTCTATGCTAGATAGTGGCAATATGGAGACTCAGCAGTGGAGACACAGGAAA 288

QY 181 ATATCCCAAAATTCAGATTATC 204
 |||||
 Db 289 GATATCCCAAAATTCAGATTATC 312

RESULT 8
 AAT64901
 ID AAT64901 standard; DNA; 2540 BP.
 AC AAT64901;
 XX
 DT 07-NOV-2000 (first entry)
 XX
 DE Human X-linked inhibitor of apoptosis DNA.
 XX
 KW X-linked inhibitor of apoptosis; XIAP; hILP; MIHA; U45880;
 KW antisense; antinflammatory; cytostatic; tumour; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 34..1527
 FT /*tag= a
 FT /product= "X-linked inhibitor of apoptosis"
 XX
 XX US6087173-A.
 XX
 PD 11-JUL-2000.
 XX
 XX 09-SEP-1999; 99US-0392580.
 PF
 XX 09-SEP-1999; 99US-0392580.
 PR
 XX (ISIS-) ISIS PHARM INC.
 XX
 XX Bennett CF, Cowser LM, Ackermann EJ;
 PI WPI; 2000-498201/44.
 DR P-PSDB; AAY99985.
 XX
 XX Antisense compound useful for research reagents, diagnostics,
 PT prophylaxis and for treating disorders associated with X-linked
 PT inhibitor of apoptosis, modulates expression of X-linked inhibitor of
 PT apoptosis
 XX
 PS Example 13; Column 43-48; 33pp; English.
 XX
 CC The present invention relates to antisense oligonucleotides designed to
 CC inhibit expression of the human X-linked inhibitor of apoptosis. The
 CC present sequence is the X-linked inhibitor of apoptosis DNA.
 CC Modified phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are
 CC more effective inhibitors than unmodified oligonucleotides. The
 CC oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis
 CC expression in cells and tissues in vitro. The oligonucleotides are also
 CC useful for treating animals or humans, prone to a disease associated
 CC with X-linked inhibitor of apoptosis. The oligonucleotides may also be
 CC used prophylactically to prevent infection, inflammation or tumour
 CC formation.
 XX
 XX Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 other;
 SQ

Query Match 84.3%; Score 172; DB 21; Length 2540;
 Best Local Similarity 90.2%; Pred. No. 4.9e-50;
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATAAAACATTTGCTAACCTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
 |||||
 Db 109 GAGTTTAATAGATAAAACATTTGCTAACCTCCCAAGTAGTAGTCTGTTTCAGCATCA 168
 |||||
 QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGTGAAGGAGACACCGTGCAATGTTTCAGT 120
 |||||
 Db 169 ACATGGCAGCAGCAGGTTCTTTATCTACTGTTGAAGAGATACCGTGCGGTGCTTTAGT 228
 |||||
 QY 121 TGTGATGGGCAATAGATAGATGCGACTGAGAGACTGAGTGTGGAAGACACAGGAGA 180
 |||||
 Db 229 TGTGATGGGCAATAGATAGATGCGACTGAGAGACTGAGTGTGGAAGACACAGGAGA 288
 |||||
 QY 181 ATATCCCCCAATTCAGATTATC 204
 |||||
 Db 289 GTATCCCCCAATTCAGATTATC 312
 |||||

RESULT 9
 ABK93869
 ID ABK93869 standard; cDNA; 2540 BP.
 XX
 AC ABK93869;
 XX
 XX
 DT 26-AUG-2002 (first entry)
 XX
 DE Human cDNA encoding inhibitor of apoptosis, XIAP #1.
 XX
 KW Human; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Homo sapiens.
 XX
 XX
 PN WO200226968-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-CA01379.
 XX
 PR 28-SEP-2000; 2000US-0672717.
 XX
 XX (UYOT-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 XX Korneeluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX WPI; 2002-479562/51.
 DR P-PSDB; ABG65663.
 XX
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for
 PT enhancing apoptosis in a cell, for treating cancer and other
 PT proliferative diseases -
 XX
 PS Disclosure; Flg 1; 135pp; English.
 XX
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (1) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic

CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC cDNA sequence.
 XX
 SQ Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;
 Query Match 84.3%; Score 172; DB 24; Length 2540;
 Best Local Similarity 90.2%; Pred. No. 4.9e-50;
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 GAGTTTAATAGATAAAACATTTGCTAACCTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
 |||||
 Db 109 GAGTTTAATAGATAAAACATTTGCTAACCTCCCAAGTAGTAGTCTGTTTCAGCATCA 168
 |||||
 QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGTGAAGGAGACACCGTGCAATGTTTCAGT 120
 |||||
 Db 169 ACATGGCAGCAGCAGGTTCTTTATCTACTGTTGAAGAGATACCGTGCGGTGCTTTAGT 228
 |||||
 QY 121 TGTGATGGGCAATAGATAGATGCGACTGAGAGACTGAGTGTGGAAGACACAGGAGA 180
 |||||
 Db 229 TGTGATGGGCAATAGATAGATGCGACTGAGAGACTGAGTGTGGAAGACACAGGAGA 288
 |||||
 QY 181 ATATCCCCCAATTCAGATTATC 204
 |||||
 Db 289 GTATCCCCCAATTCAGATTATC 312
 |||||

RESULT 10
 ABK93875
 ID ABK93875 standard; cDNA; 3000 BP.
 XX
 AC ABK93875;
 XX
 XX
 DT 26-AUG-2002 (first entry)
 XX
 DE Human cDNA encoding inhibitor of apoptosis, XIAP #2.
 XX
 KW Human; ss: gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX
 OS Homo sapiens.
 XX
 XX
 PN WO200226968-A2.
 XX
 PD 04-APR-2002.
 XX
 PF 27-SEP-2001; 2001WO-CA01379.
 XX
 PR 28-SEP-2000; 2000US-0672717.
 XX
 XX (UYOT-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX
 XX Korneeluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX WPI; 2002-479562/51.
 DR
 XX
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for
 PT enhancing apoptosis in a cell, for treating cancer and other
 PT proliferative diseases -
 XX
 PS Example 2; Flg 15; 135pp; English.
 XX
 CC The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (1) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of

CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a human IAP
 CC cDNA sequence.

XX
 SQ Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 other;

Query Match 84.3%; Score 172; DB 24; Length 3000;
 Best Local Similarity 90.2%; Pred. No. 5.3e-50;
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTACTCTGTTTCAGCATCA 60
 DB 765 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTACTCTGTTTCAGCATCA 824
 QY 61 ACATTGGCGGAGCTGGTCTTTATACCGGTGAAGGAGACACCGTCAATGTTTCAGT 120
 DB 825 ACATGGCAGCAGCAGGTTCTTTATACGTGGTGAAGGAGATACCGTGGGTGCTTTAGT 884
 QY 121 TGTCTATGGGCAATAGATAGATGCGTATGAGAGTCACTGTTTGAAGACACAGGAGA 180
 DB 885 TGTCTATGGGCAATAGATAGATGCGTATGAGAGTCACTGTTTGAAGACACAGGAGA 944
 QY 181 ATATCCCAAAATTCAGATTATC 204
 DB 945 GTATCCCAAAATTCAGATTATC 968

RESULT 11
 AAV55038
 ID AAV55038 standard; cDNA; 5232 BP.

XX
 AC AAV55038;
 XX
 DT 13-NOV-1998 (first entry)
 XX Human XIAP coding sequence.

XX
 KW Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.
 XX Homo sapiens.

XX Key Location/Qualifiers
 FH 34..1527
 FT CDS /*tag= a
 FT /product= XIAP

XX W09835693-A2.
 XX 20-AUG-1998.
 XX 13-FEB-1998; 98WO-IB00781.
 XX 13-FEB-1997; 97US-0800929.
 XX (UYOT-) UNIV OTTAWA.

XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
 FI Tsang B;
 XX WPI; 1998-467164/40.
 DR P-PSDB; AAW69294.

PT Inducing apoptosis in proliferative mammalian cells with inhibitor
 PT of IAP or NAIP polypeptide - also methods for prognosis based on
 PT presence of IAP and NAIP, specifically applied to cancers involving
 PT p53 mutations
 XX
 PS Cialm 13; Fig 1; 147pp; English.
 XX
 CC This sequence encodes the human XIAP protein, which is an inhibitor of
 CC apoptosis protein (IAP), and can be used in the method of the invention.
 CC The method is for enhancing apoptosis in cells from a mammal with
 CC proliferative disease by treatment with a compound that inhibits
 CC biological activity of an IAP or NAIP polypeptide. The inhibitory
 CC compounds are used to treat proliferative diseases, specially cancers of
 CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
 CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,
 CC rectum, cervix or endometrium, particularly to increase their sensitivity
 CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
 CC detected in many cancers and are associated with poor prognosis,
 CC resistance to chemotherapeutic agents and mutations in p53 (it is
 CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
 CC genes). Transgenic animals are used for testing the effects of antisense
 CC oligonucleotides and for screening for the inhibitors.

XX SQ Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;

Query Match 84.3%; Score 172; DB 19; Length 5232;
 Best Local Similarity 90.2%; Pred. No. 6.8e-50;
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTACTCTGTTTCAGCATCA 60
 DB 109 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTACTCTGTTTCAGCATCA 168
 QY 61 ACATTGGCGGAGCTGGTCTTTATACCGGTGAAGGAGACACCGTCAATGTTTCAGT 120
 DB 169 ACATGGCAGCAGCAGGTTCTTTATACGTGGTGAAGGAGATACCGTGGGTGCTTTAGT 228
 QY 121 TGTCTATGGGCAATAGATAGATGCGTATGAGAGTCACTGTTTGAAGACACAGGAGA 180
 DB 229 TGTCTATGGGCAATAGATAGATGCGTATGAGAGTCACTGTTTGAAGACACAGGAGA 288
 QY 181 ATATCCCAAAATTCAGATTATC 204
 DB 289 GTATCCCAAAATTCAGATTATC 312

RESULT 12
 ABL54307
 ID ABL54307 standard; DNA; 7990 BP.

XX
 AC ABL54307;
 XX
 DT 29-JUL-2002 (first entry)
 XX Chemically treated apoptosis gene #4.

XX Apoptosis; HIV; Bloom syndrome; cardiopathy;
 KW neurodegenerative disorder; Herpes simplex virus; renal ischaemia;
 KW amyotrophic lateral sclerosis; cancer; ds.
 XX Unidentified.

XX W0200177164-A2.
 XX 18-OCT-2001.
 XX 06-APR-2001; 2001WO-EP03969.

XX 06-APR-2000; 2000DE-1019058.
 PR 07-APR-2000; 2000DE-1019173.
 PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.

PA (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2002-017444/02.
 XX Chemically modified sequences of genes associated with apoptosis are
 PT useful to determine methylation patterns of genomic DNA samples for
 PT diagnosis of associated diseases such as cancer
 XX
 PS Claim 1; Seq ID #7; 24pp; English.
 CC
 CC This invention relates to chemically pre-treated DNA of genes
 CC associated with apoptosis. The nucleic acids are used to allocate
 CC patients for specific therapy for HIV infection, Bloom syndrome,
 CC cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus
 CC infection, renal ischaemia, anyotrophic lateral sclerosis, solid tumours
 CC and cancers. This nucleotide sequence represents a chemically
 CC treated apoptosis gene. Even SEQ ID numbers are the complementary
 CC DNA strands to the odd SEQ ID numbers. The sequence data for this
 CC patent is not represented in the printed specification but is based on
 CC information supplied by the European patent office.
 XX
 SQ Sequence 7990 BP; 2223 A; 102 C; 1567 G; 4098 T; 0 other;
 Query Match 62.6%; Score 127.8; DB 24; Length 7990;
 Best Local Similarity 76.8%; Pred. No. 3.1e-34;
 Matches 156; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
 QY 1 GAGTTTAATAGATAAACAATTTGCTTAACCTCCCAAGTAGTCTGTTTCAGCATCA 60
 Db 5109 GAGTTTAATAGATAAACAATTTGCTTAACCTCCCAAGTAGTCTGTTTCAGCATCA 5168
 QY 61 ACATTGGCGGAGCTGGGTTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120
 Db 5169 ATATTGGTACGAGTAGGGTTTTTTTATATTGTTGAAGGAGATATCGTCGGGTGTTTAGT 5228
 QY 121 TGTCTATGGCGCAATAGATAGTGCAGTATGAGACTCAGCTGTTTGAAGACACAGGAGA 180
 Db 5229 TGTATGTAGTGTAGATAGATGTAATATGGAGATTAGTATGTTGAAGATATAGGAAA 5288
 QY 181 ATATCCCAAAATTCAGATTAT 203
 Db 5289 GTATTTTAAATTTAGATTAT 5311
 RESULT 13
 ABL32158
 ID ABL32158 standard; DNA; 7990 BP.
 AC ABL32158;
 XX
 XX 26-MAR-2002 (first entry)
 DT
 XX
 DE Human immune system associated gene SEQ ID NO: 131.
 XX
 KW Human; Immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; antihaemic; cytostatic; nootropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antineumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 PN WO200200928-A2.
 XX
 XX 03-JAN-2002.
 PD
 XX
 XX 02-JUL-2001; 2001WO-EP07537.
 PF
 XX

PR 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX (EPIG-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2002-130909/17.
 XX Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation
 XX
 PS Claim 1; SEQ ID NO 131; 32pp + Sequence Listing; German.
 CC
 CC The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention.
 XX
 SQ Sequence 7990 BP; 2223 A; 102 C; 1567 G; 4098 T; 0 other;
 Query Match 62.6%; Score 127.8; DB 24; Length 7990;
 Best Local Similarity 76.8%; Pred. No. 3.1e-34;
 Matches 156; Conservative 0; Mismatches 47; Indels 0; Gaps 0;
 QY 1 GAGTTTAATAGATAAACAATTTGCTTAACCTCCCAAGTAGTCTGTTTCAGCATCA 60
 Db 5109 GAGTTTAATAGATAAACAATTTGCTTAACCTCCCAAGTAGTCTGTTTCAGCATCA 5168
 QY 61 ACATTGGCGGAGCTGGGTTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120
 Db 5169 ATATTGGTACGAGTAGGGTTTTTTTATATTGTTGAAGGAGATATCGTCGGGTGTTTAGT 5228
 QY 121 TGTCTATGGCGCAATAGATAGTGCAGTATGAGACTCAGCTGTTTGAAGACACAGGAGA 180
 Db 5229 TGTATGTAGTGTAGATAGATGTAATATGGAGATTAGTATGTTGAAGATATAGGAAA 5288
 QY 181 ATATCCCAAAATTCAGATTAT 203
 Db 5289 GTATTTTAAATTTAGATTAT 5311
 RESULT 14
 ABL54308/c
 ID ABL54308 standard; DNA; 7990 BP.
 XX
 XX ABL54308;
 AC
 XX
 XX 29-JUL-2002 (first entry)
 DT
 XX
 DE Chemically treated apoptosis gene complementary to gene #4.
 XX
 KW Apoptosis; HIV; Bloom syndrome; cardiopathy;
 KW neurodegenerative disorder; Herpes simplex virus;
 KW anyotrophic lateral sclerosis; cancer; ds.
 XX
 OS Unidentified.
 XX
 PN WO200177164-A2.
 XX
 XX 18-OCT-2001.
 PD
 XX
 XX 06-APR-2001; 2001WO-EP03969.
 PF
 XX
 XX 06-APR-2000; 2000DE-1019058.
 PR
 XX 07-APR-2000; 2000DE-1019173.
 PR
 XX 30-JUN-2000; 2000DE-1032529.
 PR
 XX 01-SEP-2000; 2000DE-1043826.
 PR

XX PA (EPIC-) EPIGENOMICS AG.
 XX PI Olek A, Piepenbrock C, Berlin K;
 XX XX WPI; 2002-017444/02.
 XX Chemically modified sequences of genes associated with apoptosis are
 PT useful to determine methylation patterns of genomic DNA samples for
 PT diagnosis of associated diseases such as cancer
 XX Claim 1; Seq ID #8; 24pp; English.
 XX This invention relates to chemically pre-treated DNA of genes
 CC associated with apoptosis. The nucleic acids are used to allocate
 CC patients for specific therapy for HIV infection, Bloom syndrome,
 CC cardiopathy, aging, neurodegenerative disorders, Herpes simplex virus
 CC infection, renal ischaemia, amyotrophic lateral sclerosis, solid tumours
 CC and cancers. This nucleotide sequence represents a chemically
 CC treated apoptosis gene. Even SEQ ID numbers are the complementary
 CC DNA strands to the odd SEQ ID numbers. The sequence data for this
 CC patent is not represented in the printed specification but is based on
 CC information supplied by the European patent office.
 XX
 SQ Sequence 7990 BP; 2539 A; 102 C; 1661 G; 3688 T; 0 other;
 Query Match 54.0%; Score 110.2; DB 24; Length 7990;
 Best Local Similarity 71.4%; Pred. No. 5e-28;
 Matches 145; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
 QY 2 AGTTTAATAGATTAAACATTTGCTTAACCTCCCAAGTAGTGTCTTTTCAGCATCAA 61
 Db 2881 AATTTAATAATTAACATTTTACTAATTTTCCAAATATATCTCTATTTCACATCAA 2822
 QY 62 CATTTGGCGGAGTGGGTTCTTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGTT 121
 Db 2821 CACTAACACGCAACAAATTTCTTTATCTAATAAAAAAATACCGTACGATCTTAATT 2762
 QY 122 GTCATGGCGCAATAGATAGTGGCAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGAA 181
 Db 2761 ATCATACACTATAATAAATACAAATATAAAACTCAACAATTAAAAACACAAAAA 2702
 QY 182 TATCCCCAAATTCGAGATTTATC 204
 Db 2701 TATCCCCAAATTCACAAATTTATC 2679
 RESULT 15
 ID ABL32159/C
 XX ABL32159 standard; DNA; 7990 BP.
 AC ABL32159;
 XX
 XX 26-MAR-2002 (first entry)
 XX Human immune system associated gene SEQ ID NO: 132.
 DE
 XX Human; immune system disease; cytosine methylation; antiasthmatic;
 KW antiarteriosclerotic; anti-anaemic; cytostatic; nootropic;
 KW neuroprotective; anti-HIV; anticonvulsant; ophthalmological;
 KW antirheumatic; antiarthritic; antidiabetic; antipsoriatic;
 KW antiinflammatory; cancer; eye disease; arteriosclerosis; anaemia;
 KW acute myeloid leukaemia; Alzheimer's disease; AIDS; epilepsy;
 KW neurofibromatosis; rheumatoid arthritis; psoriasis; bowel disease;
 KW gene; ds.
 XX
 OS Homo sapiens.
 XX
 XX WO200200928-A2.
 PN
 XX 03-JAN-2002.
 XX
 XX 02-JUL-2001; 2001WO-EP07537.
 PF

XX 30-JUN-2000; 2000DE-1032529.
 PR 01-SEP-2000; 2000DE-1043826.
 XX (EPIC-) EPIGENOMICS AG.
 XX Olek A, Piepenbrock C, Berlin K;
 XX WPI; 2002-130909/17.
 XX Nucleic acid comprising fragment of chemically modified gene, useful
 PT for diagnosis and treatment of diseases associated with abnormal
 PT cytosine methylation
 XX
 PS Claim 1; SEQ ID NO 132; 32pp + Sequence Listing; German.
 XX The present invention provides a number of human immune system associated
 CC genes which are modified by the methylation of cytosines. The sequences
 CC can be used in the diagnosis and treatment of immune system disorders,
 CC including eye diseases such as retinopathy, neovascular glaucoma and
 CC macular degeneration, arteriosclerosis, anaemia, cancer, acute myeloid
 CC leukaemia, Alzheimer's disease, AIDS, epilepsy, neurofibromatosis,
 CC rheumatoid arthritis, psoriasis and inflammatory/ulcerative bowel
 CC diseases. The present sequence is a gene of the invention.
 XX
 SQ Sequence 7990 BP; 2539 A; 102 C; 1661 G; 3688 T; 0 other;
 Query Match 54.0%; Score 110.2; DB 24; Length 7990;
 Best Local Similarity 71.4%; Pred. No. 5e-28;
 Matches 145; Conservative 0; Mismatches 58; Indels 0; Gaps 0;
 QY 2 AGTTTAATAGATTAAACATTTGCTTAACCTCCCAAGTAGTGTCTTTTCAGCATCAA 61
 Db 2881 AATTTAATAATTAACATTTTACTAATTTTCCAAATATATCTCTATTTCACATCAA 2822
 QY 62 CATTTGGCGGAGTGGGTTCTTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGTT 121
 Db 2821 CACTAACACGCAACAAATTTCTTTATCTAATAAAAAAATACCGTACGATCTTAATT 2762
 QY 122 GTCATGGCGCAATAGATAGTGGCAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGAA 181
 Db 2761 ATCATACACTATAATAAATACAAATATAAAACTCAACAATTAAAAACACAAAAA 2702
 QY 182 TATCCCCAAATTCGAGATTTATC 204
 Db 2701 TATCCCCAAATTCACAAATTTATC 2679
 Search completed: April 15, 2003, 21:45:37
 Job time : 143.354 secs

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:16:42 ; Search time 25.6771 seconds
(without alignments)
2436.494 Million cell updates/sec

Title: US-09-654-743-49
Perfect score: 204
Sequence: 1 gagtttaagattataaac.....ccccaaattgcagattatc 204

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/ptodata/1/ina/6B_COMB.seq: *
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6: /cgn2_6/ptodata/1/ina/backfiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	204	100.0	2100	2	US-08-511-485-9
2	204	100.0	2691	3	US-09-212-971-9
3	204	100.0	2691	3	US-08-800-929A-9
4	204	100.0	2691	4	US-09-617-053A-9
5	172	84.3	1588	4	US-09-239-867-3
6	172	84.3	2540	2	US-08-511-485-3
7	172	84.3	2540	3	US-09-392-580-1
8	172	84.3	5232	3	US-09-212-971-3
9	172	84.3	5232	3	US-08-800-929A-3
10	172	84.3	5232	4	US-09-617-053A-3
11	60.6	29.7	2862	4	US-08-569-749-13
12	60.6	29.7	2862	5	PCT-US96-12860-13
13	60.6	29.7	3151	3	US-09-212-971-13
14	60.6	29.7	3151	3	US-08-800-929A-13
15	60.6	29.7	3151	4	US-09-617-053A-13
16	59	28.9	2580	2	US-08-511-485-7
17	59	28.9	2589	4	US-08-569-749-1
18	59	28.9	2589	5	PCT-US96-12860-1
19	59	28.9	3532	2	US-09-205-204-1
20	59	28.9	3732	3	US-09-212-971-7
21	59	28.9	3732	3	US-08-800-929A-7
22	59	28.9	3732	4	US-09-617-053A-7
23	55.8	27.4	2676	3	US-09-212-971-11
24	55.8	27.4	2676	3	US-08-800-929A-11
25	55.8	27.4	2676	4	US-09-617-053A-11
26	54.4	26.7	2676	2	US-08-511-485-5
27	54.4	26.7	3076	2	US-09-205-144-1

28	54.4	26.7	6669	3	US-09-212-971-5	Sequence 5, Appl1
29	54.4	26.7	6669	3	US-08-800-929A-5	Sequence 5, Appl1
30	54.4	26.7	6669	4	US-09-617-053A-5	Sequence 5, Appl1
31	54.2	26.6	1559	4	US-09-239-867-1	Sequence 1, Appl1
32	52.8	25.9	2601	4	US-08-569-749-3	Sequence 3, Appl1
33	52.8	25.9	2601	5	PCT-US96-12860-3	Sequence 3, Appl1
34	47.6	23.3	5502	3	US-08-836-134-1	Sequence 1, Appl1
35	47.6	23.3	5502	4	US-09-493-784-1	Sequence 1, Appl1
36	42.4	20.8	1435	5	PCT-US95-05922A-1	Sequence 1, Appl1
c 37	29.8	14.6	10079	2	US-08-476-868-20	Sequence 20, Appl1
38	28.6	14.0	711	3	US-09-121-979-3	Sequence 3, Appl1
39	28.6	14.0	711	4	US-09-332-319-3	Sequence 3, Appl1
40	28.6	14.0	2343	4	US-09-484-970B-119	Sequence 119, App
41	28.6	14.0	9520	4	US-08-952-127-11	Sequence 11, Appl
c 42	28.4	13.9	168575	4	US-09-426-290-1	Sequence 1, Appl1
c 43	28	13.7	529	4	US-09-602-877A-103	Sequence 103, App
44	28	13.7	1481	1	US-08-136-922-1	Sequence 1, Appl1
45	28	13.7	2601	1	US-08-121-713D-53	Sequence 53, Appl

ALIGNMENTS

RESULT 1
US-08-511-485-9
; Sequence 9, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: MacKenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match 100.0%; Score 204; DB 2; Length 2100;
Best Local Similarity 100.0%; Pred. No. 2.7e-60;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAAACATTGCTAACCTCCCAAGTAGTAGTCCTGTTTCAGCATCA 60
|||||

Db 202 GAGTTTAATAGATTAATAAACATTGCTACTTCCCAAGTAGTAGTCTCTTTTCAGCATCA 261
QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120
Db 262 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 321
QY 121 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTTGGAAGACACAGGAGA 180
Db 322 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTTGGAAGACACAGGAGA 381
QY 181 ATATCCCCAAATTCAGATTATC 204
Db 382 ATATCCCCAAATTCAGATTATC 405

RESULT 2

US-09-212-971-9
; Sequence 9, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-212-971-9

Query Match 100.0%; Score 204; DB 3; Length 2691;
Best Local Similarity 100.0%; Pred. No. 3e-60;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAATAAACATTGCTACTTCCCAAGTAGTAGTCTCTTTTCAGCATCA 60
Db 747 GAGTTTAATAGATTAATAAACATTGCTACTTCCCAAGTAGTAGTCTCTTTTCAGCATCA 806
QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120
Db 807 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 866
QY 121 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTTGGAAGACACAGGAGA 180
Db 867 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTTGGAAGACACAGGAGA 926
QY 181 ATATCCCCAAATTCAGATTATC 204
Db 927 ATATCCCCAAATTCAGATTATC 950

RESULT 3

US-08-800-929A-9
; Sequence 9, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G

; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2691 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-800-929A-9

Query Match 100.0%; Score 204; DB 3; Length 2691;
Best Local Similarity 100.0%; Pred. No. 3e-60;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAATAAACATTGCTACTTCCCAAGTAGTAGTCTCTTTTCAGCATCA 60
Db 747 GAGTTTAATAGATTAATAAACATTGCTACTTCCCAAGTAGTAGTCTCTTTTCAGCATCA 806
QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120
Db 807 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 866
QY 121 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTTGGAAGACACAGGAGA 180
Db 867 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTTGGAAGACACAGGAGA 926
QY 181 ATATCCCCAAATTCAGATTATC 204
Db 927 ATATCCCCAAATTCAGATTATC 950

RESULT 4

US-09-617-053A-9
; Sequence 9, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 9
LENGTH: 2691
TYPE: DNA
ORGANISM: Mus musculus
US-09-617-053A-9

Query Match 100.0%; Score 204; DB 4; Length 2691;
Best Local Similarity 100.0%; Pred. No. 3e-60;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATAAACAATTTGCTAATCTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
DB 747 GAGTTTAATAGATAAACAATTTGCTAATCTCCCAAGTAGTAGTCTGTTTCAGCATCA 806

QY 61 ACATTGGCGGAGTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120
DB 807 ACATTGGCGGAGTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 866

QY 121 TGTCATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
DB 867 TGTCATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 926

QY 181 ATATCCCAAAATTCAGATTATC 204
DB 927 ATATCCCAAAATTCAGATTATC 950

RESULT 5
US-09-239-867-3
Sequence 3, Application US/09239867
Patent No. 6331412
GENERAL INFORMATION:
APPLICANT: Robert G. Korneluk et al.
TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
TITLE OF INVENTION: MALE FERTILITY
FILE REFERENCE: 07891/018002
CURRENT APPLICATION NUMBER: US/09/239,867
CURRENT FILING DATE: 1999-01-29
PRIOR APPLICATION NUMBER: 60/073,001
PRIOR FILING DATE: 1998-01-29
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 1588
TYPE: DNA
ORGANISM: Homo sapiens
US-09-239-867-3

Query Match 84.3%; Score 172; DB 4; Length 1588;
Best Local Similarity 90.2%; Pred. No. 2.1e-49;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATAAACAATTTGCTAATCTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
DB 109 GAGTTTAATAGATAAACAATTTGCTAATCTCCCAAGTAGTAGTCTGTTTCAGCATCA 168

QY 61 ACATTGGCGGAGTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120
DB 169 ACATTGGCGGAGTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCGGTGCTTAGT 228

QY 121 TGTCATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
DB 229 TGTCATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 288

QY 181 ATATCCCAAAATTCAGATTATC 204

DB 169 ACATTGGCGGAGTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCGGTGCTTAGT 228
QY 121 TGTCATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
DB 229 TGTCATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 288

QY 181 ATATCCCAAAATTCAGATTATC 204
DB 289 GATATCCCAAAATTCAGATTATC 312

RESULT 6
US-08-511-485-3
Sequence 3, Application US/08511485
Patent No. 591912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESS: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2540 base pairs.
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)
US-08-511-485-3

Query Match 84.3%; Score 172; DB 2; Length 2540;
Best Local Similarity 90.2%; Pred. No. 2.5e-49;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATAAACAATTTGCTAATCTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
DB 109 GAGTTTAATAGATAAACAATTTGCTAATCTCCCAAGTAGTAGTCTGTTTCAGCATCA 168

QY 61 ACATTGGCGGAGTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCAATGTTTCAGT 120
DB 169 ACATTGGCGGAGTGGTTCCTTTATACCGGTGAAGGAGACACCGTGCGGTGCTTAGT 228

QY 121 TGTCATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
DB 229 TGTCATCGGCAATAGATAGATGCGAGTATGGAGACTCAGCTGTTGGAAGACACAGGAGA 288

QY 181 ATATCCCAAAATTCAGATTATC 204

REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 5232 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: Other

LOCATION: 1...5232

OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.

US-08-800-929A-3

Query Match 84.3%; Score 172; DB 3; Length 5232;

Best Local Similarity 90.2%; Pred. No. 3.4e-49;

Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACATTTGCTAAGTCTCCCAAGTAGTAGTCTGTTTCAGCATCA 60

DB 109 GAGTTTAATAGATTAAACACATTTGCTAAGTCTCCCAAGTAGTAGTCTGTTTCAGCATCA 168

QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120

DB 169 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 228

QY 121 TGTCTATCGCGCAATAGATAGATGCGAGTATGGAGACTGAGTCTGTTGAAGACACAGGAGA 180

DB 229 TGTCTATCGCGCAATAGATAGATGCGAGTATGGAGACTGAGTCTGTTGAAGACACAGGAGA 288

QY 181 ATATCCCAAAATTCGAGATTATC 204

DB 289 GTATCCCAAAATTCGAGATTATC 312

RESULT 10

US-09-617-053A-3

Sequence 3, Application US/09617053A

Patent No. 6300492

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G

APPLICANT: Mackenzie, Alexander E

APPLICANT: Liston, Peter

APPLICANT: Baird, Stephen

APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND

TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

TITLE OF INVENTION: DISEASE

FILE REFERENCE: 07891/009003

CURRENT APPLICATION NUMBER: US/09/617,053A

PRIOR FILING DATE: 2000-07-14

PRIOR APPLICATION NUMBER: US 08/800,929

PRIOR FILING DATE: 1997-02-13

NUMBER OF SEQ ID NOS: 17

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 5232

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: variation

LOCATION: (4623)...(4623)

OTHER INFORMATION: n can be any nucleotide

NAME/KEY: variation

LOCATION: (4622)...(4622)

OTHER INFORMATION: n can be any nucleotide

US-09-617-053A-3

Query Match 84.3%; Score 172; DB 4; Length 5232;
Best Local Similarity 90.2%; Pred. No. 3.4e-49;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACATTTGCTAAGTCTCCCAAGTAGTAGTCTGTTTCAGCATCA 60

DB 109 GAGTTTAATAGATTAAACACATTTGCTAAGTCTCCCAAGTAGTAGTCTGTTTCAGCATCA 168

QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120

DB 169 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 228

QY 121 TGTCTATCGCGCAATAGATAGATGCGAGTATGGAGACTGAGTCTGTTGAAGACACAGGAGA 180

DB 229 TGTCTATCGCGCAATAGATAGATGCGAGTATGGAGACTGAGTCTGTTGAAGACACAGGAGA 288

QY 181 ATATCCCAAAATTCGAGATTATC 204

DB 289 GTATCCCAAAATTCGAGATTATC 312

RESULT 11

US-08-569-749-13

Sequence 13, Application US/08569749

Patent No. 6187557

GENERAL INFORMATION:

APPLICANT: Roche, Mike

APPLICANT: Goeddel, David V

TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

NUMBER OF SEQUENCES: 14

CORRESPONDENCE ADDRESS:

ADDRESSEE: FLEHR, HOEBACH, TEST, ALBRITTON & HERBERT

STREET: 4 Embarcadero Center, Suite 3400

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111

COMPUTER READABLE FORM: disk

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/569,749

FILING DATE:

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Brezner, David J.

REGISTRATION NUMBER: 24,774

REFERENCE/DOCKET NUMBER: A-62464/DJB

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)781-1989

TELEFAX: (415)398-3249

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

LENGTH: 2862 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

US-08-569-749-13

Query Match 29.7%; Score 60.6; DB 4; Length 2862;

Best Local Similarity 56.2%; Pred. No. 3.3e-11;

Matches 114; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACACATTTGCTAAGTCTCCCAAGTAGTAGTCTGTTTCAGCATCA 60

DB 608 GAATCTACCGAATGTCTACATATTACGTTTCCCGAGGCGAGTCTGTTCTCAGAGAGG 667

QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGT 120

DB 668 AGTCTGGCTGCTGGCTTTTATTATACAGGTGTGAATGACAAAGTCAAGTCTTCTGTC 727

QY 121 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGAAGACACAGGAGA 180
Db 728 TGTGGCCTGATGTGGTAACTGGAACAAAGGGGACAGTCTCTGTGAAAGACACAGAG 787
QY 181 ATATCCCAAAATTGCAGATTAT 203
Db 788 TTCTATCCAGCTGCAGCTTTGT 810

RESULT 12
PCT-US96-12860-13
; Sequence 13, Application PC/TUS9612860
; GENERAL INFORMATION:
; APPLICANT: TULARIK, INC.
; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOEACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/12860
; FILING DATE: 06 AUG 1996
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Brezner, David J.
; REGISTRATION NUMBER: 24,774
; REFERENCE/DOCKET NUMBER: A-62464/DOJ
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)781-1989
; TELEFAX: (415)398-3249
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2862 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
PCT-US96-12860-13

Query Match 29.7%; Score 60.6; DB 5; Length 2862;
Best Local Similarity 56.2%; Pred. No. 3 se-11;
Matches 114; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAAACATTGTGTAACCTCCCAAGTAGTAGTCTCTGTTCCAGCATCA 60
Db 608 GAACTCTACCGAATGTCTACATATTCAGCTTTTCCCGAGGGAGCTTCTGTCTCAGAGAG 667
QY 61 ACATTGCGCGAGCTGGTTCCTTTATACCGGTGAAGGACACACCGTGCATGTTTCAGT 120
Db 668 AGTCTGGCTGCTGGCTTTTATTATACAGGTGTGAATGACAAAGTCAAGTCTCTCTGC 727
QY 121 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGAAGACACAGGAGA 180
Db 728 TGTGGCCTGATGTGGTAACTGGAACAAAGGGGACAGTCTCTGTGAAAGACACAGAG 787
QY 181 ATATCCCAAAATTGCAGATTAT 203
Db 788 TTCTATCCAGCTGCAGCTTTGT 810

RESULT 13
US-09-212-971-13
; Sequence 13, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; CURRENT FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 3151
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-212-971-13

Query Match 29.7%; Score 60.6; DB 3; Length 3151;
Best Local Similarity 56.2%; Pred. No. 3 se-11;
Matches 114; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
QY 1 GAGTTTAATAGATTAAACATTGTGTAACCTCCCAAGTAGTAGTCTCTGTTCCAGCATCA 60
Db 914 GAACTCTACCGAATGTCTACATATTCAGCTTTTCCCGAGGGAGTCTGTCTCAGAGAG 973
QY 61 ACATTGCGCGAGCTGGTTCCTTTATACCGGTGAAGGACACACCGTGCATGTTTCAGT 120
Db 974 AGTCTGGCTGCTGGCTTTTATTATACAGGTGTGAATGACAAAGTCAAGTCTCTCTGC 1033
QY 121 TGTCTATGCGGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGAAGACACAGGAGA 180
Db 1034 TGTGGCCTGATGTGGTAACTGGAACAAAGGGGACAGTCTCTGTGAAAGACACAGAG 1093
QY 181 ATATCCCAAAATTGCAGATTAT 203
Db 1094 TTCTATCCAGCTGCAGCTTTGT 1116

RESULT 14
US-08-800-929A-13
; Sequence 13, Application US/08800929A
; Patent No. 6133437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERA
; TITLE OF INVENTION: DISEASE
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Elbing LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA

```
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3151 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-800-929A-13

Query Match          29.7%  Score 60.6; DB 3; Length 3151;
Best Local Similarity 56.2%  Pred. No. 3.5e-11;
Matches 114; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 1 GAGTTTAAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
   || || || || || || || || || || || || || || || || || || || || ||
Db 914 GAACTCTACCGAATGCTACATATTTCAGCTTTTCCAGGGGAGTTCTGTCTCAGAGAGG 973

QY 61 ACATTGGGGGAGCTGGGTTTCTTTATACCGGTGAAGGAGACACCGTGCATATGTTTCAGT 120
   || || || || || || || || || || || || || || || || || || || || ||
Db 974 AGTCTGGCTCGTGGCTTTTATTATACAGGTGTGAATGACAAAGTCAAGTGTCTCTGC 1033

QY 121 TGTCAATGGGCAATAGATAGATGCGAGTATGAGACTCAGCTGTTGGAAGACACAGGAGA 180
   || || || || || || || || || || || || || || || || || || || || ||
Db 1034 TGTGGCTGTATGTTGGATACTGGAACACAGGGGACAGTCTCTGTTGAAAACACAGACAG 1093

QY 181 ATATCCCAAAATTCAGATTTAT 203
   || || || || || || || || || || || || || || || || || || || || ||
Db 1094 TTCTATCCAGCTGCAGCTTTGT 1116

Search completed: April 16, 2003, 00:58:54
Job time : 28.6771 secs
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Query Match          29.7%  Score 60.6; DB 3; Length 3151;
Best Local Similarity 56.2%  Pred. No. 3.5e-11;
Matches 114; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 1 GAGTTTAAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
   || || || || || || || || || || || || || || || || || || || || ||
Db 914 GAACTCTACCGAATGCTACATATTTCAGCTTTTCCAGGGGAGTTCTGTCTCAGAGAGG 973

QY 61 ACATTGGGGGAGCTGGGTTTCTTTATACCGGTGAAGGAGACACCGTGCATATGTTTCAGT 120
   || || || || || || || || || || || || || || || || || || || || ||
Db 974 AGTCTGGCTCGTGGCTTTTATTATACAGGTGTGAATGACAAAGTCAAGTGTCTCTGC 1033

QY 121 TGTCAATGGGCAATAGATAGATGCGAGTATGAGACTCAGCTGTTGGAAGACACAGGAGA 180
   || || || || || || || || || || || || || || || || || || || || ||
Db 1034 TGTGGCTGTATGTTGGATACTGGAACACAGGGGACAGTCTCTGTTGAAAACACAGACAG 1093

QY 181 ATATCCCAAAATTCAGATTTAT 203
   || || || || || || || || || || || || || || || || || || || || ||
Db 1094 TTCTATCCAGCTGCAGCTTTGT 1116

RESULT 15
US-09-617-053A-13
; Sequence 13, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
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Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	204	100.0	2100	9	US-09-201-936-9		Sequence 9, Appl
2	204	100.0	2691	10	US-09-974-592-9		Sequence 9, Appl
3	172	84.3	2404	9	US-09-964-899-38		Sequence 38, Appl
4	172	84.3	2540	9	US-09-201-936-3		Sequence 3, Appl
5	172	84.3	5232	10	US-09-974-592-3		Sequence 3, Appl
6	60.6	29.7	2416	9	US-09-201-936-41		Sequence 41, Appl
7	60.6	29.7	3151	10	US-09-974-592-13		Sequence 13, Appl
8	59	28.9	2580	9	US-09-201-936-7		Sequence 7, Appl
9	59	28.9	3532	10	US-09-880-107-3354		Sequence 3354, Ap
10	59	28.9	3732	10	US-09-974-592-7		Sequence 7, Appl
11	57.4	28.1	2291	10	US-09-978-927A-21		Sequence 21, Appl
12	55.8	27.4	2450	9	US-09-201-936-39		Sequence 39, Appl
13	55.8	27.4	2676	10	US-09-974-592-11		Sequence 11, Appl
14	54.4	26.7	2676	9	US-09-201-936-5		Sequence 5, Appl
15	54.4	26.7	3076	9	US-09-954-531-16		Sequence 16, Appl
16	54.4	26.7	3076	10	US-09-934-456-1635		Sequence 1635, Ap
17	54.4	26.7	6669	10	US-09-974-592-5		Sequence 5, Appl
18	47.6	23.3	5504	8	US-08-913-342-1		Sequence 1, Appl
19	47.6	23.3	6124	8	US-08-913-342-1		Sequence 21, Appl

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QY 121 TGTCTATGGCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGAAGACACAGGAGA 180
      |||||||
Db 322 TGTCTATGGCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGAAGACACAGGAGA 381
      |||||||

QY 181 ATATCCCAAAATTGCAGATTATC 204
      |||||||
Db 382 ATATCCCAAAATTGCAGATTATC 405
      |||||||

RESULT 2
US-09-974-592-9
; Sequence 9, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US/09/974,592
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-974-592-9

Query Match 100.0%; Score 204; DB 10; Length 2691;
Best Local Similarity 100.0%; Pred. No. 1.9e-61;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTCTGTTTCAGCATCA 60
      |||||||
Db 747 GAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTCTGTTTCAGCATCA 806
      |||||||

QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCCGTCGAATGTTTCAGT 120
      |||||||
Db 807 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCCGTCGAATGTTTCAGT 866
      |||||||

QY 121 TGTCTATGGCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGAAGACACAGGAGA 180
      |||||||
Db 867 TGTCTATGGCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGAAGACACAGGAGA 926
      |||||||

QY 181 ATATCCCAAAATTGCAGATTATC 204
      |||||||
Db 927 ATATCCCAAAATTGCAGATTATC 950
      |||||||

RESULT 3
US-09-964-899-38
; Sequence 38, Application US/09964899
; Patent No. US2002017446A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Dalia et al.
; TITLE OF INVENTION: Identification of Genes Involved in
; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
; FILE REFERENCE: 4-31612 A
; CURRENT APPLICATION NUMBER: US/09/964,899
; CURRENT FILING DATE: 2001-09-27
; PRIOR APPLICATION NUMBER: 60/236,893
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: 60/298,309
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; PRIOR FILING DATE: 2001-06-14
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
; LENGTH: 2404
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-964-899-38

Query Match 84.3%; Score 172; DB 9; Length 2404;
Best Local Similarity 90.2%; Pred. No. 3.3e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTCTGTTTCAGCATCA 60
      |||||||
Db 109 GAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTCTGTTTCAGCATCA 168
      |||||||

QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCCGTCGAATGTTTCAGT 120
      |||||||
Db 169 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCCGTCGAATGTTTCAGT 228
      |||||||

QY 121 TGTCTATGGCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGAAGACACAGGAGA 180
      |||||||
Db 229 TGTCTATGGCGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTGTGAAGACACAGGAGA 288
      |||||||

QY 181 ATATCCCAAAATTGCAGATTATC 204
      |||||||
Db 289 ATATCCCAAAATTGCAGATTATC 312
      |||||||

RESULT 4
US-09-201-936-3
; Sequence 3, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3

Query Match 84.3%; Score 172; DB 9; Length 2540;
Best Local Similarity 90.2%; Pred. No. 3.4e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTCTGTTTCAGCATCA 60
      |||||||
Db 109 GAGTTTAATAGATTAAAAACATTTGCTAACTTCCCAAGTAGTAGTCTCTGTTTCAGCATCA 168
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QY 61 ACATTGGCGGAGCTGGGTTCTTTATACCGGTGAAGAGACACCCGTCGAATGTTTCAGT 120
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; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT FILING DATE: 1998-12-01
; CURRENT APPLICATION NUMBER: US/09/201.936
; EARLIER FILING DATE: 1998-02-04
; EARLIER FILING DATE: 1998-02-04
; EARLIER FILING DATE: 1996-08-05
; EARLIER FILING DATE: 1995-12-22
; EARLIER FILING DATE: 1995-12-22
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-201-936-41

Query Match      29.7%; Score 60.6; DB 9; Length 2416;
Best Local Similarity 56.2%; Pred. No. 5.6e-11;
Matches 114; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTACCTGTTTCAGCATCA 60
Db 215 GAAGTCTACCGAATGCTACATATTTCAGCTTTTCCAGGGAGTTCTCTGTCAGAGAGG 274

QY 61 ACATGGCGGAGCTGGGTTTCTTTATACCGTGAAGGAGACACGGTGCATGTTTCAGT 120
Db 275 AGTCTGGCTCGTGTGGCTTTTATATACAGGTGTGAATGACAAAGTCAAGTGTCTGTC 334

QY 121 TGTCATCGGCAATAGATAGATGGCAGTATGGAGTATGAGTGGAGACACAGGAGAGA 180
Db 335 TGTGCGCTGATGTTGGATACTGGAACACAGGGGACAGCTCTGTTGAAAGCACAGACAG 394

QY 181 ATATCCCAAAATTCAGATTTAT 203
Db 395 TTCTATCCAGCTGCAGCTTTGT 417

RESULT 7
US-09-974-592-13
; Sequence 13, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; FILE REFERENCE: 07891/009004
; CURRENT FILING DATE: 2001-10-09
; CURRENT APPLICATION NUMBER: US/09/974.592
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 3151
; TYPE: DNA

; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT FILING DATE: 1998-12-01
; CURRENT APPLICATION NUMBER: US/09/201.936
; EARLIER FILING DATE: 1998-02-04
; EARLIER FILING DATE: 1998-02-04
; EARLIER FILING DATE: 1996-08-05
; EARLIER FILING DATE: 1995-12-22
; EARLIER FILING DATE: 1995-12-22
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-201-936-41

Query Match      84.3%; Score 172; DB 10; Length 5232;
Best Local Similarity 90.2%; Pred. No. 5e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTACCTGTTTCAGCATCA 60
Db 109 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTACCTGTTTCAGCATCA 168

QY 61 ACATGGCGGAGCTGGGTTTCTTTATACCGTGAAGGAGACACGGTGCATGTTTCAGT 120
Db 169 ACATGGCGGAGCTGGGTTTCTTTATACCGTGAAGGAGATACCGTGCAGTGTTCAGT 228

QY 121 TGTCATCGGCAATAGATAGATGGCAGTATGGAGTATGAGTGGAGACACAGGAGAGA 180
Db 229 TGTCATCGCTGTAGATAGATGGCAATATGGAGACTCAGCAGTGGAGACACAGGAAA 288

QY 181 ATATCCCAAAATTCAGATTTATC 204
Db 289 GTATCCCAAAATTCAGATTTATC 312

RESULT 6
US-09-201-936-41
; Sequence 41, Application US/09201936
; Publication No. US20020187946A1
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; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE REFERENCE: 07891/003003
; CURRENT FILING DATE: 1998-12-01
; CURRENT APPLICATION NUMBER: US/09/201.936
; EARLIER FILING DATE: 1998-02-04
; EARLIER FILING DATE: 1998-02-04
; EARLIER FILING DATE: 1996-08-05
; EARLIER FILING DATE: 1995-12-22
; EARLIER FILING DATE: 1995-12-22
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 41
; LENGTH: 2416
; TYPE: DNA
; ORGANISM: Mus musculus
; US-09-201-936-41

Query Match      29.7%; Score 60.6; DB 9; Length 2416;
Best Local Similarity 56.2%; Pred. No. 5.6e-11;
Matches 114; Conservative 0; Mismatches 89; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATTAAACATTTGCTAACTTCCCAAGTAGTACCTGTTTCAGCATCA 60
Db 215 GAAGTCTACCGAATGCTACATATTTCAGCTTTTCCAGGGAGTTCTCTGTCAGAGAGG 274

QY 61 ACATGGCGGAGCTGGGTTTCTTTATACCGTGAAGGAGACACGGTGCATGTTTCAGT 120
Db 275 AGTCTGGCTCGTGTGGCTTTTATATACAGGTGTGAATGACAAAGTCAAGTGTCTGTC 334

QY 121 TGTCATCGGCAATAGATAGATGGCAGTATGGAGTATGAGTGGAGACACAGGAGAGA 180
Db 335 TGTGCGCTGATGTTGGATACTGGAACACAGGGGACAGCTCTGTTGAAAGCACAGACAG 394

QY 181 ATATCCCAAAATTCAGATTTAT 203
Db 395 TTCTATCCAGCTGCAGCTTTGT 417

RESULT 7
US-09-974-592-13
; Sequence 13, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; FILE REFERENCE: 07891/009004
; CURRENT FILING DATE: 2001-10-09
; CURRENT APPLICATION NUMBER: US/09/974.592
; PRIOR FILING DATE: 2000-07-14
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13
; LENGTH: 3151
; TYPE: DNA
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QY	1	GAGTTTAATAGATTAAACATTTGCTAACTTTCCCAAGTAGTAGTCCTGGTTTTCAGCATCA	60
Db	373	GAACCTACAGAAATGTCTACATAATTCAACTTTCCC CGCGGGTGCTGTCTCAGAAAGG	432
QY	61	ACATTGCCGCGAGCTGGGTTCTTTTATACCGGTGAAGGAGACACCGTCGCAATGTTTCAGT	120
Db	433	AGTCTTTGCTCGTGTGGTTTTTATTATAGTGGTGTGAATGCACAGGTCAAATGCTTCTGT	492
QY	121	TGTCATGCGCGAATAGATAGATGGCAGTATCGAGACTCAGCTGTTGGGAAGACACAGGAGA	180
Db	493	TGTGGCTCATCTGGATAACTGGAACTAGGAGACAGTCTTATTCAAAAGCATTAACAG	552

```

: GENERAL INFORMATION:
:
: APPLICANT: Korneluk, Robert G
: APPLICANT: Mackenzie, Alexander E
: APPLICANT: Liston, Peter
: APPLICANT: Baird, Stephen
: APPLICANT: Tsang, Benjamin K
: APPLICANT: Pratt, Christine
:
: TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
: TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT
: TITLE OF INVENTION: DISEASE
: FILE REFERENCE: 07891/009004
:
: CURRENT APPLICATION NUMBER: US/09/974,592
: CURRENT FILING DATE: 2001-10-09
: PRIOR APPLICATION NUMBER: US 09/617,053
: PRIOR FILING DATE: 2000-07-14

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PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 3732
TYPE: DNA
ORGANISM: Homo sapiens
US-09-974-592-7

Query Match 28.9%; Score 59; DB 10; Length 3732;

Best Local Similarity 55.7%; Pred. No. 2.6e-10;

Matches 113; Conservative 0; Mismatches 90; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATAAACAATTTGCTAAGTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
DB 1515 GAACCTACAGATGCTCATATATCAACTTCCCGCGGGGCTGCTCAGAAAG 1574
QY 61 ACATTGGCGGAGCTGGGTTTCTTTATACCGGTGAAGGAGACACCGTCAATGTTTCAGT 120
DB 1575 ACTCTGCTGCTGGTGTATATATCTGTTGTTGATGACAGAGTCAATGCTTCTGT 1634
QY 121 TGTGATCGGCAATAGATAGATGAGCAGTATGGAGCTAGCTGTTGGAAGACACAGGAGA 180
DB 1635 TGTGGCTGATGCTGGATAACTGGAACTAGGAGACAGTCTCTATTCAAAGCATAAACAG 1694
QY 181 ATATCCCAAAATTCAGATTAT 203
DB 1695 CTATATCTAGCTAGCTTTAT 1717

RESULT 11

US-09-778-927A-21
Sequence 21, Application US/09778927A
Patent No. US20020068342A1

GENERAL INFORMATION:

APPLICANT: KHOSRAVI, Rami et al.

TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL

FILE REFERENCE: 2786-0160P

CURRENT APPLICATION NUMBER: US/09/778,927A

PRIOR APPLICATION NUMBER: IL 134453

PRIOR FILING DATE: 2000-02-09

PRIOR FILING DATE: 2000-03-29

NUMBER OF SEQ ID NOS: 81

SOFTWARE: Patent In Ver. 2.1

SEQ ID NO 21

LENGTH: 2291

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc.feature

LOCATION: (1)-(2291)

OTHER INFORMATION: n - a, c, g, t any unknown or other

US-09-778-927A-21

Query Match 28.1%; Score 57.4; DB 10; Length 2291;

Best Local Similarity 55.2%; Pred. No. 7.3e-10;

Matches 112; Conservative 0; Mismatches 91; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATAAACAATTTGCTAAGTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
DB 1508 GAACCTACAGATGCTCATATATCAACTTCCCGCGGGGCTGCTCAGAAAG 1567
QY 61 ACATTGGCGGAGCTGGTTCCTTTATACCGGTGAAGGAGACACCGTCAATGTTTCAGT 120
DB 1568 AGTCTGCTGCTGGTGTCTATATATCTGTTGTTGATGACAGAGTCAATGTTCTGT 1627
QY 121 TGTGATCGGCAATAGATAGATGAGCAGTATGGAGCTAGCTGTTGGAAGACACAGGAGA 180
DB 1628 TGTGGCTGATGCTGGATAACTGGAACTAGGAGACAGTCTCTATTCAAAGCATAAACAG 1687

QY 181 ATATCCCAAAATTCAGATTAT 203
DB 1688 CTATATCTAGCTAGCTTTAT 1710

RESULT 12

US-09-201-936-39

Sequence 39, Application US/09201936

PATENT NO. US20020187946A1

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: Mackenzie, Alexander E.

APPLICANT: Baird, Stephen

APPLICANT: Liston, Peter

TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,

FILE REFERENCE: 07891/003003

CURRENT APPLICATION NUMBER: US/09/201,936

EARLIER FILING DATE: 1998-12-01

EARLIER FILING DATE: 1998-02-04

EARLIER FILING DATE: 1996-08-05

EARLIER FILING DATE: 1995-12-22

EARLIER FILING DATE: 1995-08-04

NUMBER OF SEQ ID NOS: 45

SOFTWARE: FASTSEQ for Windows Version 3.0

SEQ ID NO 39

LENGTH: 2450

TYPE: DNA

ORGANISM: Mus musculus

US-09-201-936-39

Query Match 27.4%; Score 55.8; DB 9; Length 2450;

Best Local Similarity 54.7%; Pred. No. 2.8e-09;

Matches 111; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 1 GAGTTTAATAGATAAACAATTTGCTAAGTCCCAAGTAGTAGTCTGTTTCAGCATCA 60
DB 240 GAGCTGTACCGATTGTCACGCTATTCAGCTTTCCAGGGGAGTCTCTGTGTCAGAAAG 299
QY 61 ACATTGGCGGAGCTGGTTCCTTTATACCGGTGAAGGAGACACCGTCAATGTTTCAGT 120
DB 300 AGTCTGCTGCTGCTGCTTTTACTACACTGCTGCTCAATGACAAAGTCAAGTCTCTGC 359
QY 121 TGTGATCGGCAATAGATAGATGAGCAGTATGGAGCTAGCTGTTGGAAGACACAGGAGA 180
DB 360 TGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 419
QY 181 ATATCCCAAAATTCAGATTAT 203
DB 420 TTGTACCCAGCTGCAACTTTGT 442

RESULT 13

US-09-974-592-11

Sequence 11, Application US/09974592

PATENT NO. US20020120121A1

GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.

APPLICANT: Mackenzie, Alexander E.

APPLICANT: Liston, Peter

APPLICANT: Baird, Stephen

APPLICANT: Tsang, Benjamin K

APPLICANT: Pratt, Christine

TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND

TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

FILE REFERENCE: 07891/009004

CURRENT APPLICATION NUMBER: US/09/974,592

QY 181 ATATCCCAAAATTGCAGATT 200
Db 989 TTGTAACCTAGCTGCAGATT 1008

Search completed: April 16, 2003, 01:03:52
Job time : 54.0521 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:12:47 ; Search time 976.083 Seconds
(without alignments)
3384.833 Million cell updates/sec

Title: US-09-654-743-49
Perfect score: 204
Sequence: 1 gagtttaagattataaac.....ccccaaattgcagatttattc 204

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum:*
3: em_estlin:*
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5: em_estov:*
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10: gb_est2:*
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12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
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16: em_estom:*
17: gb_gss:*
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25: em_gssOther:*
26: em_gsspro:*
27: em_gssrod:*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	200.8	98.4	698	10	BB653654
2	172	84.3	529	9	AL713196
3	172	84.3	1041	13	BM459898
4	161	78.9	852	14	BQ423165
5	108.2	53.0	822	12	BG502660
6	98.6	48.3	575	13	BM489612

7	93.2	45.7	603	9	AL646185
8	90.2	44.2	676	13	BI392530
9	85.2	41.8	593	13	BJ096099
10	85.2	41.8	681	12	BF611032
11	84.2	41.3	530	13	BJ030180
12	78.8	38.6	603	12	BF614726
13	75	36.8	624	14	BQ552033
14	68	33.3	567	13	BI475879
15	68	33.3	552	13	BI706974
16	68	33.3	565	13	BI706975
17	68	33.3	676	12	BF156225
18	66.4	32.5	574	13	BI706911
19	65.8	32.3	746	9	AF160669
20	62.6	30.7	300	9	AU098645
21	60.6	29.7	633	12	BE912864
22	59	28.9	464	14	BM753271
23	59	28.9	837	12	BG743309
24	59	28.9	855	9	AU131149
25	59	28.9	891	12	BE886741
26	58.6	28.7	613	14	BQ391082
27	58.6	28.7	644	14	BQ389388
28	58	28.4	600	13	BM539590
29	58	28.4	823	12	BG572956
30	57.2	28.0	535	14	BQ618784
31	57.2	28.0	594	12	BF158160
32	57.2	28.0	658	13	BM157229
33	56.8	27.8	801	13	BG934097
34	55.8	27.4	569	12	BG082235
35	55.8	27.4	669	10	BB625247
36	54.8	26.9	756	12	BG73530
37	54.4	26.7	590	10	AW500255
38	54.4	26.6	959	13	BM458775
39	54.2	26.6	742	13	BI829221
40	54.2	26.6	884	13	BI104522
41	54.2	26.6	1020	13	BM545444
42	54.2	26.6	1130	13	BM553272
43	54	26.5	230	10	BE164141
44	53.6	26.3	384	9	AL843873
45	52.8	25.9	475	12	BF615511

ALIGNMENTS

RESULT 1	BB653654	698 bp	mRNA	linear	EST 26-OCT-2001
LOCUS	BB653654	RIKEN full-length enriched, adult male liver tumor Mus			
DEFINITION	BB653654	cDNA clone C730014L18 5', mRNA sequence.			
ACCESSION	BB653654				
VERSION	BB653654.1	GI:16487482			
KEYWORDS	EST.				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
	1 (bases 1 to 698)				
	Arakawa,T., Carninci,P., Fukuda,S., Furuno,M., Hanagaki,T., Hara,A., Hiramoto,K., Hori,F., Ishii,Y., Ito,M., Kawai,J., Konno,H., Kouda,M., Koya,S., Matsuyama,T., Miyazaki,A., Namura,K., Ono,M., Onda,O., Okazaki,Y., Okido,T., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Takeda,Y., Tanaka,T., Toya,T., Muramatsu,M. and Hayashizaki,Y.				
TITLE	RIKEN Mouse ESTs (Arakawa,T., et al. 2001)				
JOURNAL	Unpublished (2001)				
COMMENT	Contact: Yoshihide Hayashizaki				
	Laboratory for Genome Exploration Research				
	Sciences Center(GSC), Yokohama Institute				
	The Institute of Physical and Chemical Research (RIKEN)				
	1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan				
	Tel: 81-45-503-9222				
	Fax: 81-45-503-9216				

AL646185 AL646185
BI325530 pppln.pk0
BJ096099 BJ096099
BF611032 dg96h06.y
BJ030180 BJ030180
BF614726 dg96h08.y
BQ552033 H401JA06-
BI475879 fp48b06.x
BI706974 fq13c08.y
BI706975 fq13c09.y
BI706911 fq12c09.y
AF160669 D0274649
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BE912864 601665326
BM753271 K-EST0030
BG743309 602633394
AU131149 AU131149
BE886741 601506903
BQ391082 NISC.mq16
BQ389388 NISC.mq07
BM539590 hb11c10.g
BG572956 602593929
BQ618784 fdb07g12.
BM157229 fv45g04.y
BG934097 SK1-0386
BG082235 H3074A02-
BB625247 BB625247
BB625247 BB625247
AW500255 UI-HF-BNO
BM458775 AGENCOURT
BI829221 603079537
BI104522 602892537
BM545444 AGENCOURT
BM553272 AGENCOURT
BE164141 QV2-HF046
AL843873 AL843873
BF615511 de08a04.y

Email: genome-res@gsc.riken.go.jp.
 URL: http://genome.gsc.riken.go.jp/
 Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh
 M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 Normalization and subtraction of cap-trapper-selected cDNAs to
 prepare full-length cDNA libraries for rapid discovery of new
 genes. Genome Res. 10 (10), 1617-1630 (2000)
 wagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E.,
 Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura
 S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and
 Hayashizaki, Y.
 RIKEN integrated sequence analysis (RISA) system--384-format
 sequencing pipeline with 384 multicapillary sequencer. Genome Res.
 10 (11), 1757-1771 (2000)
 Konno, H., Fukunishi, Y., Shibata, K., Itoh, M., Carninci, P., Sugahara
 Y. and Hayashizaki, Y.
 Computer-based methods for the mouse full-length cDNA
 encyclopedia: real-time sequence clustering for construction of a
 nonredundant cDNA library. Genome Res. 11 (2), 281-289 (2001)
 Kondo, S., Shinagawa, A., Saito, T., Kiyosawa, H., Yamanaka, I., Aizawa
 K., Fukuda, S., Hara, A., Itoh, M., Kawai, J., Shibata, K. and
 Hayashizaki, Y.
 Computational Analysis of Full-Length Mouse cDNAs Compared with
 Human Genome Sequences. Mamm. Genome. 12, 673-677 (2001)
 Please visit our web site (http://genome.gsc.riken.go.jp) for
 further details.
 e mouse tissues.

FEATURES

Location/Qualifiers

source

1..698
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="C73001418"
 /clone_lib="RIKEN full-length enriched, adult male liver
 tumor"
 /sex="male"
 /tissue_type="liver tumor"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Site 1: Sali; Site 2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN. Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5'
 GAGAGAGAGCGCGCAACTCGAGTTTCTTTTCTTTT 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence [5'
 GAGAGAGAGATTCTCGAGTTAATTAATTAATCCCGCCCCC 3']. cDNA
 was cleaved with BamHI and XhoI. Vector: a modified
 pBluescript KS(+) after bulk excision from Lambda FLC I.
 Tissue was provided by William A. Held, Roswell Park
 Cancer Institute, Department of Molecular and Cellular
 Biology, Elm and Carlton Streets, Buffalo, NY 14263, whose
 assistance we gratefully acknowledge."
 167 a 163 c 170 g 197 t 1 others

BASE COUNT

ORIGIN

Query Match 98.4%; Score 200.8; DB 10; Length 698;
 Best Local Similarity 99.0%; Pred. No. 2.9e-57;
 Matches 202; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 GAGTTTAATAGATTAACAACTTGGCTAACTTCCAGTAGTAGTCTCTGTTTCAGCATCA 60
 Db 451 GAGTTTAATAGATTAACAACTTGGCTAACTTCCAGTAGTAGTCTCTGTTTCAGCATCA 510
 QY 61 ACATTGGCGGCGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGTGCATGTTTCAGT 120
 Db 511 ACATTGGCGGCGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGTGCATGTTTCAGT 570
 QY 121 TGTCTATGGCGCAATAGATAGATGCGATATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180

Db 571 TGTCTATGGCGCAATAGATAGATGCGATATGGAGACTCAGCTGTTGGAAGACACAGGAGA 630
 QY 181 ATATCCCAAAATTCGAGATTATC 204
 Db 631 ATATCCCAAAATTCGAGATTATC 654
 RESULT 2
 AL713196 529 bp mRNA linear EST 22-MAR-2002
 LOCUS DKFZP686M1895_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
 DEFINITION DKFZP686M1895_5', mRNA sequence.
 ACCESSION AL713196
 VERSION AL713196.1 GI:19696552
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 529)
 AUTHORS Bloecker, H., Boecher, M., Brandt, P., Mewes, W., Weil, B. and Wiemann
 S.
 TITLE EST (Bloecker, H., Boecher, M., Brandt, P., Mewes, H.W., Weil, B. and
 Wiemann, S.)
 JOURNAL Unpublished (1999)
 COMMENT Contact: Bloecker H
 MIPS
 Am Klopferspitz 18a D-82152 Martinsried, Germany
 This is the 5' sequence of the clone insert
 Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
 Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
 Sequenced by GBF (National Research Centre for Biotechnology Ltd.,
 Braunschweig/Germany) within the cDNA sequencing consortium of the
 German Genome Project.
 No sl sequence available.
 This clone (DKFZP686M1895) is available at the RZPD in Berlin.
 Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
 Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.
 FEATURES
 Location/Qualifiers
 source
 1..529
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="DKFZP686M1895"
 /clone_lib="886 (synonym: hlcc3)"
 /tissue_type="human skeletal muscle"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Vector: pTriplex2; Site 1: SfiIA; Site 2: SfiIB;
 cDNA-collection"
 BASE COUNT 165 a 96 c 126 g 142 t
 ORIGIN
 Query Match 84.3%; Score 172; DB 9; Length 529;
 Best Local Similarity 90.2%; Pred. No. 1.6e-47;
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 GAGTTTAATAGATTAACAACTTGGCTAACTTCCAGTAGTAGTCTCTGTTTCAGCATCA 60
 Db 137 GAGTTTAATAGATTAACAACTTGGCTAACTTCCAGTAGTAGTCTCTGTTTCAGCATCA 196
 QY 61 ACATTGGCGGCGAGCTGGGTTCTTTATACCGGTGAAGAGACACCGTGCATGTTTCAGT 120
 Db 197 ACATTGGCGGCGAGCTGGGTTCTTTATACCGGTGAAGAGATACCGTGCCTGTTTGTAGT 256
 QY 121 TGTCTATGGCGCAATAGATAGATGCGATATGGAGACTCAGCTGTTGGAAGACACAGGAGA 180
 Db 257 TGTCTATGGCGCAATAGATAGATGCGATATGGAGACTCAGCTGTTGGAAGACACAGGAGA 316
 QY 181 ATATCCCAAAATTCGAGATTATC 204
 Db 317 GTATCCCAAAATTCGAGATTATC 340

```

RESULT 3
BM459898      1041 bp      mRNA      linear      EST 05-FEB-2002
LOCUS      AGENCOURT_6422054 NIH_MGC_71 Homo sapiens cDNA clone IMAGE:5532247
DEFINITION      5', mRNA sequence.
ACCESSION      BM459898
VERSION      BM459898.1 GI:18508938
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 1041)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: ATCC
               CDNA Library Preparation: Life Technologies, Inc.
               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLAM12215 row: d column: 08
               High quality sequence stop: 567.
FEATURES      Location/Qualifiers
               source      1..1041
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:5532247"
               /clone_lib="NIH_MGC_71"
               /tissue_type="leiomyosarcoma"
               /lab_host="DH10B (phage-resistant)"
               /note="Organ: uterus; Vector: PCMV-SPORT6; Site_1: NotI;
               Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
               Average insert size 2.1 kb."
               297 a      266 g      269 t      1 others
BASE COUNT      297 a      208 c      266 g      269 t
ORIGIN
Query Match      84.38; Score 172; DB 13; Length 1041;
Best Local Similarity 90.28; Pred. No. 2.3e-47;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
QY      1 GAGTTTAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCCTGTTTCAGCATCA 60
DB      142 GAGTTTAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCCTGTTTCAGCATCA 201
QY      61 ACATGGCGGCGAGTGGGTTCTTTATACCGGTGAAGGAGACACGTCGCAATGTTTCAGT 120
DB      202 ACATGGCGGCGAGTGGGTTCTTTATACCGGTGAAGGAGATACCGTGGCGTCTTAGT 261
QY      121 TGTATGCGGCAATAGATAGATAGTGGCAGTATGGAGACTCAGCTGTTGGAGACACAGGAGA 180
DB      262 TGTATGCGGCAATAGATAGTGGCAGTATGGAGACTCAGCTGTTGGAGACACAGGAGA 321
QY      181 ATATCCCCAAATTCAGATTTATC 204
DB      322 GTATCCCCAAATTCAGATTTATC 345

RESULT 4
BQ423165
LOCUS      AGENCOURT_7761069 NIH_MGC_72 Homo sapiens cDNA clone IMAGE:6062005
DEFINITION      5', mRNA sequence.
ACCESSION      BQ423165
VERSION      BQ423165.1 GI:21118480
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 852)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: ATCC
               CDNA Library Preparation: Life Technologies, Inc.
               CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
               DNA Sequencing by: Agencourt Bioscience Corporation
               Clone distribution: MGC clone distribution information can be
               found through the I.M.A.G.E. Consortium/LLNL at:
               http://image.llnl.gov
               Plate: LLAM13332 row: m column: 14
               High quality sequence stop: 503.
FEATURES      Location/Qualifiers
               source      1..852
               /organism="Homo sapiens"
               /db_xref="taxon:9606"
               /clone="IMAGE:6062005"
               /clone_lib="NIH_MGC_72"
               /tissue_type="melanotic melanoma"
               /lab_host="DH10B (phage-resistant)"
               /note="Organ: skin; Vector: PCMV-SPORT6; Site_1: NotI;
               Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
               Average insert size 2 kb. Library constructed by Life
               Technologies."
               210 a      191 c      242 g      209 t
BASE COUNT      210 a      191 c      242 g      209 t
ORIGIN
Query Match      78.98; Score 161; DB 14; Length 852;
Best Local Similarity 89.88; Pred. No. 1.2e-43;
Matches 184; Conservative 0; Mismatches 20; Indels 1; Gaps 1;
QY      1 GAGTTTAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCCTGTTTCAGCATCA 60
DB      398 GAGTTTAATAGATAAAACATTTGCTAACTTCCCAAGTAGTAGTCCTGTTTCAGCATCA 457
QY      61 ACATGGCGGCGAGTGGGTTCTTTATACCGGTGAAGGAGACACGTCGCAATGTTTCAGT 120
DB      458 ACATGGCGGCGAGTGGGTTCTTTATACCGGTGAAGGAGATACCGTGGCGTCTTAGT 517
QY      121 TGTATGCGGCAATAGATAGATAGTGGCAGTATGGAGACTCAGCTGTTGGAGACACAGGAGA 180
DB      518 TGTATGCGGCAATAGATAGTGGCAGTATGGAGACTCAGCTGTTGGAGACACAGGAGA 577
QY      181 ATAT-CCCCAAATTCAGATTTATC 204
DB      578 GTATCCCCAAATTCAGATTTATC 602

RESULT 5
BG502660      822 bp      mRNA      linear      EST 27-MAR-2001
LOCUS      602549490P1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4657102 5',
DEFINITION      mRNA sequence.
ACCESSION      BG502660
VERSION      BG502660.1 GI:13464177
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 822)
AUTHORS      NIH-MGC http://mgc.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
               Email: cgapbs-r@mail.nih.gov
               Tissue Procurement: ATCC
               CDNA Library Preparation: CLONETECH Laboratories, Inc.

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w7,w9)"
/lab_host="E. Coli EMDH10B"
/note="vector: pCMVSPORT6; Library made from equivalent
pools of total RNA isolated from each tissue at different
ages. Single pass sequencing from 5'-end"
BASE COUNT      141 a   156 c   194 g   166 t   19 others
ORIGIN
Query Match      44.2%; Score 90.2; DB 13; Length 676;
Best Local Similarity 64.8%; Pred. No. 1.4e-19;
Matches 125; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 11 GATTAAACAATTGCTAACTCCCAAGTAGTAGCTCTGTTTCAGGATCAACATTGGCGC 70
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 419 GACTAGGAACCTTTGTGGAGTTTCCCATGATTCTCCAGATTCAGCATCAGCGGTAGCTC 478
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 71 GAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGGTGCAATGTTTCAGTTGTCTATGCGG 130
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 479 GAGCTGGCTTTGTTTATCTACGGAGAGAGTGTAAGTCAAGTCTTCAGTTGCCATGTAA 538
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 131 CAATGATAGATGAGCATGTGGAGACATGAGCTGTTGGAAGACACAGGAGAATATCCCAA 190
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 539 CTGTTGAAGATGGAGCCCTNNNGCATTTCTGCAATTGACAGACACAAAAACCTTNNNCNAG 598
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 191 ATTGCAGATTAT 203
| | | | | | | | | |
Db 599 NNGCAGATTAT 611
| | | | | | | | | |

RESULT 9
BJ096099
LOCUS
DEFINITION
BJ096099 NIBB Mochii normalized xenopus early gastrula library
Xenopus laevis cDNA clone XLI52K19 5', mRNA sequence.
ACCESSION
BJ096099
VERSION
BJ096099.1 GI:17596868
KEYWORDS
EST.
SOURCE
BJ096099.1 African clawed frog.
Xenopus laevis
Xenopus laevis
Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
Xenopodinae; Xenopus.
REFERENCE
1 (bases 1 to 593)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-i,T. and Kohara
,Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-i
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
Location/Qualifiers
1..593
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XLI52K19"
/clone_lib="NIBB Mochii normalized xenopus early gastrula
library"
/tissue_type="whole embryo"
/dev_stage="stage 10.5"
/note="vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Newkooop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."
BASE COUNT      175 a   129 c   137 g   152 t
ORIGIN
Query Match      41.8%; Score 85.2; DB 13; Length 593;
Best Local Similarity 64.9%; Pred No. 6.5e-18;

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Matches 126; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 10 AGATTAACAACTTCTAATCCCAAGTAGTAGTCTGTTTCAGCATCAACATGGCG 69
DB 54 AGACTGGCCCTCTTCTAATTTCAAGTAGTAGTACCCCTGTTCTGCCCCAGCAGTAGCA 113
QY 70 CGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGTTGTCATGGC 129
DB 114 CGGCGCGGCTTTTATACACTGGAGATGGAGACCGAGTAAGTGTGTTTACGTGTATGGCT 173
QY 130 GCAATAGATAGATGGAGTATGAGACTGAGTGTGGAGACAGAGAGATATCCCA 189
DB 174 ATGGTCGAAGATGGAGATGGAGACACCGCAATCGGCAAGCATCGGAATATCTCCA 233
QY 190 AATTGCAGATTAT 203
DB 234 AACTGTAATTCAT 247

RESULT 10
LOCUS BF611032 681 bp mRNA linear EST 14-DEC-2000
DEFINITION d96h06.y1 Wellcome CRC PRN3 oocyte Xenopus laevis cDNA clone
IMAGE:3436642 5' similar to SW:IAPI3_MOUSE Q60989 INHIBITOR OF
APOPTOSIS PROTEIN 3 ; , mRNA sequence.
ACCESSION BF611032
VERSION BF611032.1 GI:11780268
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 681)
Clifton,S., Johnson,S.L., Blumberg,B., Song,J., Hillier,L., Pape,D.,
Martin,J., Wylie,T., Underwood,K., Theising,B., Bowers,Y., Person
,B., Gibbons,M., Harvey,N., Ritter,E., Jackson,Y., McCann,R.,
Waterston,R. and Wilson,R.
Washu Xenopus EST project, 1999
Unpublished (1999)
Other ESTs: dd96h06.x1
Contact: Sandy Clifton, Ph.D.
Washu Xenopus EST project, 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.edu
Library constructed by N. Garrett, P. LeMaire, A.M. Zorn, and J.B.
Gurdon (Wellcome/CRC Institute). DNA Sequencing by: Washington
University Genome Sequencing Center
Clone distribution: Xenopus clones from this library are available
through the I.M.A.G.E. Consortium/LLNL at: info@image.llnl.gov
Seq primer: -40bp from Gibco
High quality sequence stop: 513.
FEATURES
source
location/Qualifiers
1..681
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="IMAGE:3436642"
/clone_lib="Wellcome CRC PRN3 oocyte"
/tissue_type="oocyte"
/lab_host="DH10B (phage-resistant)"
/notes="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library was constructed
by N. Garrett, P. LeMaire, A.M. Zorn, and J.B. Gurdon
(Wellcome/CRC Institute)."
BASE COUNT 198 a 149 c 155 g 177 t 2 others
Query Match 41.8%; Score 85.2; DB 12; Length 681;
Best Local Similarity 64.9%; Pred. No. 7e-18;

Matches 126; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 10 AGATTAACAACTTCTAATCCCAAGTAGTAGTCTGTTTCAGCATCAACATGGCG 69
DB 54 AGACTGGCCCTCTTCTAATTTCAAGTAGTAGTACCCCTGTTCTGCCCCAGCAGTAGCA 113
QY 70 CGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGTTGTCATGGC 129
DB 114 CGGCGCGGCTTTTATACACTGGAGATGGAGACCGAGTAAGTGTGTTTACGTGTATGGCT 173
QY 130 GCAATAGATAGATGGAGTATGAGACTGAGTGTGGAGACAGAGAGATATCCCA 189
DB 174 ATGGTCGAAGATGGAGATGGAGACACCGCAATCGGCAAGCATCGGAATATCTCCA 233
QY 190 AATTGCAGATTAT 203
DB 234 AACTGTAATTCAT 247

RESULT 11
LOCUS BJ030180 530 bp mRNA linear EST 05-DEC-2001
DEFINITION BJ030180 NIBB Mochii normalized Xenopus neurula library Xenopus
laevis cDNA clone XL003f24 5', mRNA sequence.
ACCESSION BJ030180
VERSION BJ030180.1 GI:17371606
KEYWORDS EST.
SOURCE African clawed frog.
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 530)
Kitayama,A., Terasaka,C., Mochii,M., Ueno,N., Shin-I,T. and Kohara
,Y.
Expressed genes in X. laevis embryo
Unpublished (2001)
Contact: Tadasu Shin-I
Center For Genetic Resource Information
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshini@genes.nig.ac.jp.
FEATURES
source
location/Qualifiers
1..530
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="XL003f24"
/clone_lib="NIBB Mochii normalized Xenopus neurula
library"
/tissue_type="whole embryo"
/dev_stage="stage 15"
/notes="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
were oligo-dT primed and directionally cloned. Staging
according to Nieuwkoop and Faber. Library is subtracted
and was constructed by N. Garrett and A.M. Zorn,
(Wellcome/CRC Institute)."
BASE COUNT 156 a 112 c 125 g 136 t 1 others
Query Match 41.3%; Score 84.2; DB 13; Length 530;
Best Local Similarity 64.4%; Pred. No. 1.3e-17;
Matches 125; Conservative 0; Mismatches 69; Indels 0; Gaps 0;
QY 10 AGATTAACAACTTGTGAATCTCCCAAGTAGTAGTCTGTTTCAGCATCAACATGGCG 69
DB 126 AGACTGGCCCTCTTCTAATTTCAAGTAGTAGTACCCCTGTTCTGCCCCAGCAGTAGCA 185
QY 70 CGAGCTGGGTTCTTTATACCGGTGAAGGAGACACCGTGCATGTTTCAGTTGTCATGGC 129
DB 186 CGGCGCGGCTTTTATACACTGGAGATGGAGACCGAGTAAGTGTATAGTGTATGGCT 245

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QY 129 GGCAATAGATAGATGGCAGTATGGAGACTCAGCTGTTGGAAAGACACAGGAGGAATATCCCC 188
Db 157 GACTGCTGACAACTGGCAGTCTGTGACTGTCCCGCAGAGCGCCACAAACAGCTATCCCC 216
QY 189 AAATTGCAGATTTATC 204
Db 217 CAACTGCAGCTTCATC 232

Search completed: April 16, 2003, 00:55:03
Job time : 1978.083 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model
Run on: April 15, 2003, 19:40:42 ; Search time 1031.86 Seconds
(without alignments)
5753.635 Million cell updates/sec

Title: US-09-654-743-50
Perfect score: 204
Sequence: 1 gaagagcagattgaagtc.....ttcccaattgctttttgtt 204

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 2034640 seqs, 14551402878 residues
Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
- 13: gb.un.*
- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
- 23: em.pat.*
- 24: em.ph.*
- 25: em.pl.*
- 26: em.ro.*
- 27: em.sts.*
- 28: em.un.*
- 29: em.vi.*
- 30: em.htg_hum.*
- 31: em.htg_inv.*
- 32: em.htg_other.*
- 33: em.htg_mus.*
- 34: em.htg_pln.*
- 35: em.htg_rod.*
- 36: em.htg_mam.*
- 37: em.htg_vrt.*
- 38: em_sy.*
- 39: em_htgo_hum.*
- 40: em_htgo_mus.*
- 41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	204	100.0	2100	6	AX412124	Sequence
2	204	100.0	2691	6	AR106400	Sequence
3	204	100.0	2691	6	AR116702	Sequence
4	204	100.0	2691	10	MM088990	Mus musculus
5	202.4	99.2	1988	10	MMU36842	Mus musculus
6	178.4	87.5	2032	10	AF304333	Rattus no
7	178.4	87.5	2468	10	AB033366	Rattus no
8	178.4	87.5	3032	10	AF304334	Rattus no
9	176.8	86.7	1491	10	AF183429	Rattus no
10	172	84.3	1659	9	E31042	Method for
11	172	84.3	1659	9	HSU32974	Human IAP-1
12	172	84.3	2086	9	BC032729	Homo sapi
13	172	84.3	2540	6	AR103281	Sequence
14	172	84.3	2540	6	AX412118	Sequence
15	172	84.3	2540	9	HSU45880	Human X-link
16	172	84.3	3000	6	AX412131	Sequence
17	172	84.3	5232	6	AR106397	Sequence
18	172	84.3	5232	6	AR116699	Sequence
19	172	84.3	133391	9	HSU31561	Human DNA
20	172	84.3	201197	2	HS424312	Homo sapien
21	161	78.9	2404	6	AX429575	Sequence
22	156	76.5	1758	6	AX370787	Sequence
23	154.4	75.7	1758	6	AX370789	Sequence
24	154.4	75.7	2032	9	AF420440	Homo sapi
25	154.4	75.7	4993	6	AX104968	Sequence
26	154.4	75.7	4993	9	AF164682	Homo sapi
27	154.4	75.7	144301	9	AC010467	Homo sapi
28	154.4	75.7	165662	9	AC092070	Homo sapi
29	135.8	66.6	1740	5	AF451854	Gallus ga
30	121.8	59.7	184439	2	AP003085	Homo sapi
31	121.8	59.7	187568	9	AF002967	Homo sapi
32	120.8	59.2	7990	6	AX281265	Sequence
33	120.8	59.2	7990	6	AX345060	Sequence
34	103.8	50.9	7990	6	AX281266	Sequence
35	103.8	50.9	7990	6	AX345061	Sequence
36	81.4	39.9	2563	9	HUMSCP8	Homo sapien
37	81.4	39.9	2601	6	AR129833	Sequence
38	81.4	39.9	2676	6	AX412120	Sequence
39	81.4	39.9	2916	9	HSU45878	Human inhib
40	81.4	39.9	3076	6	AR076287	Sequence
41	81.4	39.9	3076	6	AX330574	Sequence
42	81.4	39.9	3076	6	AX334153	Sequence
43	81.4	39.9	3076	9	HSU37546	Human IAP h
44	81.4	39.9	3734	6	AX055871	Sequence
45	81.4	39.9	3734	6	AX472621	Sequence

ALIGNMENTS

RESULT 1	AX412124	2100 bp	DNA
LOCUS	Sequence 224 from Patent WO0226968.		
DEFINITION	AX412124		
ACCESSION	AX412124		
VERSION	AX412124.1	GI:21444584	
KEYWORDS	house mouse,		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
REFERENCE	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.		
AUTHORS	Korneluk, R.G., Lacasse, E., Baird, S., Holcik, M. and Young, S.		
TITLE	Antisense iap nucleic acids and uses thereof		
JOURNAL	Patent: WO 0226968-A 224 04-APR-2002;		

linear PAT 15-JUN-2002

University of Ottawa (CA) ; Aegera Therapeutics Inc. (CA)

FEATURES
source
Location/Qualifiers
1. .2100
/organism="Mus musculus"
/db_xref="taxon:10090"

BASE COUNT 615 a 417 c 482 g 586 t
ORIGIN

Query Match 100.0%; Score:204; DB 6; Length 2100;
Best Local Similarity 100.0%; Pred. No. 4.6e-52;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGACTATGCTCAATTTAACCCCCAGA 60
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Db 613 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGACTATGCTCAATTTAACCCCCAGA 672
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QY 61 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120
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Db 673 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 732
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QY 121 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 180
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Db 733 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 792
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QY 181 CACTTTCCCAATTGCTTTTGT 204
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Db 793 CACTTTCCCAATTGCTTTTGT 816
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RESULT 2

AR106400
LOCUS
DEFINITION
Sequence 9 from patent US 6107041.
ACCESSION
AR106400
VERSION
AR106400.1 GI:12820930
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 2691)
AUTHORS
Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.
TITLE
Detection and modulation of IAPs for the diagnosis and treatment of proliferative disease
JOURNAL
Patent: US 6107041-A 9 22-AUG-2000;
FEATURES
Location/Qualifiers
source
1. .2691
/organism="unknown"

BASE COUNT 819 a 479 c 562 g 831 t
ORIGIN

Query Match 100.0%; Score:204; DB 6; Length 2691;
Best Local Similarity 100.0%; Pred. No. 4.5e-52;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGACTATGCTCAATTTAACCCCCAGA 60
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QY 61 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120
|||||
Db 1218 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 1277
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QY 121 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 180
|||||
Db 1278 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 1337
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QY 181 CACTTTCCCAATTGCTTTTGT 204
|||||
Db 1338 CACTTTCCCAATTGCTTTTGT 1361
|||||

RESULT 4

MMU88990
LOCUS
DEFINITION
Mus musculus X-linked inhibitor of apoptosis (miap-3) mRNA,
complete cds.
ACCESSION
U88990
VERSION
U88990.1 GI:2138318
KEYWORDS
SOURCE
Mus musculus.
ORGANISM
Mus musculus.
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2691)
AUTHORS
Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.
TITLE
Genomic Organization and Primary Characterization of miap-3: The Murine Homologue of Human X-linked IAP
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 2691)
AUTHORS
Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.
TITLE
Direct Submission
JOURNAL
Submitted (07-FEB-1997) Molecular Genetics, Children's Hospital of Eastern Ontario, 401 Smyth Rd., Ottawa, Ontario K1H 8L1, Canada
FEATURES
Location/Qualifiers
source
1. .2691
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="X"
/map="A3-A5 region"
/dev_stage="embryo"
1. .2691
/gene="miap-3"
<1. .1545

gene
exon

AR116702
LOCUS
DEFINITION
Sequence 9 from patent US 6133437.
ACCESSION
AR116702
VERSION
AR116702.1 GI:14097024
KEYWORDS
SOURCE
Unknown.
ORGANISM
Unclassified.
REFERENCE
1 (bases 1 to 2691)
AUTHORS
Korneluk, R.G., Mackenzie, A.E., Liston, P., Baird, S., Tsang, B.K. and Pratt, C.
TITLE
Modulation of IAPs for the treatment of proliferative diseases
JOURNAL
Patent: US 6133437-A 9 17-OCT-2000;
FEATURES
Location/Qualifiers
source
1. .2691
/organism="unknown"

BASE COUNT 819 a 479 c 562 g 831 t
ORIGIN

Query Match 100.0%; Score:204; DB 6; Length 2691;
Best Local Similarity 100.0%; Pred. No. 4.5e-52;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGACTATGCTCAATTTAACCCCCAGA 60
|||||
Db 1158 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGACTATGCTCAATTTAACCCCCAGA 1217
|||||

QY 61 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120
|||||
Db 1218 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 1277
|||||

QY 121 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 180
|||||
Db 1278 TGTGGGGAAACTGAAATTTGGAACTGCTGATGCTGCTGGTGCAGAACACAGGAGA 1337
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QY 181 CACTTTCCCAATTGCTTTTGT 204
|||||
Db 1338 CACTTTCCCAATTGCTTTTGT 1361
|||||

RESULT 4

MMU88990
LOCUS
DEFINITION
Mus musculus X-linked inhibitor of apoptosis (miap-3) mRNA,
complete cds.
ACCESSION
U88990
VERSION
U88990.1 GI:2138318
KEYWORDS
SOURCE
Mus musculus.
ORGANISM
Mus musculus.
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 2691)
AUTHORS
Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.
TITLE
Genomic Organization and Primary Characterization of miap-3: The Murine Homologue of Human X-linked IAP
JOURNAL
Unpublished
REFERENCE
2 (bases 1 to 2691)
AUTHORS
Farahani, R., Lefebvre, C., Korneluk, R.G. and Mackenzie, A.E.
TITLE
Direct Submission
JOURNAL
Submitted (07-FEB-1997) Molecular Genetics, Children's Hospital of Eastern Ontario, 401 Smyth Rd., Ottawa, Ontario K1H 8L1, Canada
FEATURES
Location/Qualifiers
source
1. .2691
/organism="Mus musculus"
/db_xref="taxon:10090"
/chromosome="X"
/map="A3-A5 region"
/dev_stage="embryo"
1. .2691
/gene="miap-3"
<1. .1545

gene
exon

LOCUS AF304333 2032 bp mRNA linear ROD 19-DEC-2000
DEFINITION Rattus norvegicus clone 1 inhibitor of apoptosis protein 3 mRNA, complete cds.
ACCESSION AF304333
VERSION AF304333.1 GI:11890718
KEYWORDS Rattus norvegicus.
SOURCE Rattus norvegicus.
ORGANISM Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 2032)
AUTHORS Lareu, R.R., Bradley, C.K., Lacher, M., Friis, R.R. and Dharmarajan, A.M.
TITLE Cloning, characterization and regulation of an inhibitor of apoptosis protein in the rat corpus luteum
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2032)
AUTHORS Lareu, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.
TITLE Direct Submission
JOURNAL Submitted (08-SEP-2000) Anatomy and Human Biology, University of Western Australia, Verdm St, Nedlands, WA 6907, Australia
FEATURES Location/Qualifiers
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 /organism="Rattus norvegicus"
 /strain="Wistar"
 /db_xref="taxon:10116"
 /clone="1"
 /tissue_type="ovary"
 /note="isolated at day 15 of pregnancy"
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 /note="IAP3"
 /codon_start=1
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 /protein_id="AAG41192.1"
 /db_xref="GI:11890719"
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 STLARAGFLVTGGDTVQCFSCAAVDWQYGDVAVGRHRRISPNCFPIFYFENG
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 CSSEARLKTQNPWDYAHLSPRELASGLYTGIDDOVQCFCCGKLNWPCDRAWS
 EHRHFPCEFFVIGRNVRNRSVSGSDRNFPNSTNPRNPAEYDARIYVFTGLY
 SVNKEOLARAGFVAGLGGDKVKCFHCGGLADWKPSEDPEQHAQWYPCGKYLDEKG
 QEYINNHLTHSLGESVYVTAETKPSVTKKIDDTIFQNPVQAEIRMGFNFKDKIKTM
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 BASE COUNT 609 a 385 c 473 g 565 t
 ORIGIN
 Query Match 87.5%; Score 178.4; DB 10; Length 2032;
 Best Local Similarity 92.2%; Pred. No. 3.5e-44;
 Matches 188; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCGGAGCTATGCTCATTTAACCCCCAGA 60
 Db 611 GAAGAAGCCAGACTGAAGACGCTTCAGAACTGGCGGAGCTATGCTCATTTAACCCCCAGA 670
 QY 61 GAGTTAGTAGTGTGGCTCTACTACACAGGCGCTGATGATCAAGTCCATGCTTTGT 120
 Db 671 GAGTTAGTAGTGTGGCTCTACTACACAGGCGGATGATGATCAAGTCCATGCTTTGT 730
 QY 121 TGTGGGGAAACTCAAAAATTTGGAAACCCCTGTGATCGTCTGCTGTGCTCAGACACAGGAGA 180
 Db 731 TGTGGTGAAGAACTGAAAAATTTGGAAACCCCTGTGACCGTGTGCTGTGCTCAGACAGGAGA 790
 QY 181 CACTTTCCTCAATGCTTTTGT 204
 Db 791 CACTTTCCTCACTGCTTCTCGTT 814
RESULT 7
AB033366 2468 bp mRNA linear ROD 15-OCT-1999
LOCUS AF304334
DEFINITION Rattus norvegicus riap3 mRNA, complete cds.

ACCESSION AB033366
VERSION AB033366.1 GI:6045147
KEYWORDS RIAP3.
SOURCE Rattus norvegicus cDNA to mRNA.
ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 2468)
AUTHORS Saito, N.
TITLE Rattus norvegicus X-linked inhibitor of apoptosis (riap3) mRNA
JOURNAL Published Only in Database (1999)
REFERENCE 2 (bases 1 to 2468)
AUTHORS Saito, N.
TITLE Direct Submission
JOURNAL Submitted (07-OCT-1999) Nobuhito Saito, University of Tokyo, Department of Neurosurgery; 7-3-1 Hongo, Bunkyo-ku, Tokyo 113-8655, Japan (E-mail:nsaito-tky@umin.ac.jp, Tel:+81-3-5800-8853, Fax:+81-3-5800-8655)
FEATURES Location/Qualifiers
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 CSSEARLKTQNPWDYAHLSPRELASGLYTGIDDOVQCFCCGKLNWPCDRAWS
 EHRHFPCEFFVIGRNVRNRSVSGSDRNFPNSTNPRNPAEYDARIYVFTGLY
 SVNKEOLARAGFVAGLGGDKVKCFHCGGLADWKPSEDPEQHAQWYPCGKYLDEKG
 QEYINNHLTHSLGESVYVTAETKPSVTKKIDDTIFQNPVQAEIRMGFNFKDKIKTM
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 BASE COUNT 690 a 481 c 609 g 688 t
 ORIGIN
 Query Match 87.5%; Score 178.4; DB 10; Length 2468;
 Best Local Similarity 92.2%; Pred. No. 3.5e-44;
 Matches 188; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
 QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCGGAGCTATGCTCATTTAACCCCCAGA 60
 Db 816 GAAGAAGCCAGACTGAAGACGCTTCAGAACTGGCGGAGCTATGCTCATTTAACCCCCAGA 875
 QY 61 GAGTTAGTAGTGTGGCTCTACTACACAGGCGCTGATGATCAAGTCCATGCTTTGT 120
 Db 876 GAGTTAGTAGTGTGGCTCTACTACACAGGCGGATGATGATCAAGTCCATGCTTTGT 935
 QY 121 TGTGGGGAAACTCAAAAATTTGGAAACCCCTGTGATCGTCTGCTGTGCTCAGACACAGGAGA 180
 Db 936 TGTGGTGAAGAACTGAAAAATTTGGAAACCCCTGTGACCGTGTGCTGTGCTCAGACAGGAGA 995
 QY 181 CACTTTCCTCAATGCTTTTGT 204
 Db 996 CACTTTCCTCACTGCTTCTCGTT 1019
RESULT 8
AF304334 3032 bp mRNA linear ROD 19-DEC-2000
LOCUS AF304334
DEFINITION Rattus norvegicus clone 2 inhibitor of apoptosis protein 3 mRNA, complete cds.
ACCESSION AF304334
VERSION AF304334.1 GI:11890720
KEYWORDS Rattus norvegicus.
SOURCE Rattus norvegicus.

ORGANISM	Rattus norvegicus	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE	1 (bases 1 to 3032)	1 (bases 1 to 1491)
AUTHORS	Lareu, R.R., Bradley, C.K., Lacher, M., Friis, R.R. and Dharmarajan, A.M.	Holcik, M., Lefebvre, C.A., Hicks, K. and Korneluk, R.G.
TITLE	Cloning, characterization and regulation of an inhibitor of apoptosis protein in the rat corpus luteum	Cloning and characterization of the rat homologues of the Inhibitor of Apoptosis protein 1, 2, and 3 genes
JOURNAL	Dharmarajan, A.M.	BMC Genomics 3 (1), 5 (2002)
REFERENCE	2 (bases 1 to 3032)	2 (bases 1 to 1491)
AUTHORS	Lareu, R.R., Lacher, M., Friis, R.R. and Dharmarajan, A.M.	Holcik, M., Lefebvre, C.A., Hicks, K. and Korneluk, R.G.
TITLE	Direct Submission	Direct Submission
JOURNAL	Submitted (08-SEP-2000) Anatomy and Human Biology, University of Western Australia, Verdum St, Nedlands, WA 6907, Australia	Submitted (08-SEP-1999) Department of Biochemistry, Microbiology and Immunology, University of Ottawa, 451 Smyth Road, Ottawa, Ontario K1H 8M5, Canada
FEATURES	Location/Qualifiers	Location/Qualifiers
source	1..3032	1..1491
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	/strain="Wistar"	/db_xref="taxon:10116"
	/db_xref="taxon:10116"	1..1491
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	/notes="isolated at day 15 of pregnancy"	/product="inhibitor of apoptosis protein 3"
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	/note="IAP3"	/translation="MTNFSFGSRVTPADTNKDEEFVEFNRLKTFANFPSSPVSA
	/codon_start=1	STLARAGFLVTGEGDTVQCFSCAAVDRWYGDVAGVRRHRIISPCNRFINGFYFNGA
	/product="inhibitor of apoptosis protein 3"	TQSTSPGIQNGQYKSENCVGNRNHFALDRPSEHAYLLRTGQVVDISDIIYPRNPAM
	/protein_id="AAG41193.1"	CSEARHPCFTQNPDIYAHLSPRELASSAGLYTGIDDOVQVCCGCKLNWEPEDRAW
	/db_xref="GI:11890721"	EHRHFPNCFVILGRNVNRSVSGSDRNFPNSTSPNPRPMAEYDARIVITFTGLY
	/note="IAP3"	SVNKEQLARAGFALGEGDKVKCFHCGGLTDWKPSDPEQHAQWPGCKYLLDEKG
	/codon_start=1	QEVINNIHLTHSLGSESVVTAETKPSVTKKIDDTIFQNPVQEAIRMGFNFKDKKTM
	/product="inhibitor of apoptosis protein 3"	EKLQTSNGLSLEVLADLVSAOKNSODESSQTSLOKDIETEOQLRLQEEKLCK
	/protein_id="AAG41193.1"	ICMDNRATVFPVCGHLVTCQCAEAVDKCPMCTVTFKQFLCLNPAQ"
	/db_xref="GI:11890721"	
	/translation="MTNFSFGSRVTPADTNKDEEFVEFNRLKTFANFPSSPVSA	
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	TQSTSPGIQNGQYKSENCVGNRNHFALDRPSEHAYLLRTGQVVDISDIIYPRNPAM	
	CSEARHPCFTQNPDIYAHLSPRELASSAGLYTGIDDOVQVCCGCKLNWEPEDRAW	
	EHRHFPNCFVILGRNVNRSVSGSDRNFPNSTSPNPRPMAEYDARIVITFTGLY	
	SVNKEQLARAGFALGEGDKVKCFHCGGLTDWKPSDPEQHAQWPGCKYLLDEKG	
	QEVINNIHLTHSLGSESVVTAETKPSVTKKIDDTIFQNPVQEAIRMGFNFKDKKTM	
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BASE COUNT	817 a 657 c 688 g 870 t	464 a 282 c 357 g 388 t
ORIGIN		
Query Match	87.5%; Score 178.4; DB 10; Length 3032;	86.7%; Score 176.8; DB 10; Length 1491;
Best Local Similarity	92.2%; Pred. No. 3.4e-44;	91.7%; Pred. No. 1.1e-43;
Matches	188; Conservative 0; Mismatches 16; Indels 0; Gaps 0;	187; Conservative 0; Mismatches 17; Indels 0; Gaps 0;
Qy	1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCGGAGCTATGCTCATTTAACCCCCAGA 60	1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCGGAGCTATGCTCATTTAACCCCCAGA 60
Db	1412 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCGGAGCTATGCTCATTTAACCCCCAGA 1471	487 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCGGAGCTATGCTCATTTAACCCCCAGA 546
Qy	61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTGT 120	61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTGT 120
Db	1472 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTGT 1531	547 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTGT 606
Qy	121 TGTGGGGAAACACTGAAAAATTTGGAAACCCCTGTGATCGTGGCTGTCAGAACACAGGAGA 180	121 TGTGGGGAAACACTGAAAAATTTGGAAACCCCTGTGATCGTGGCTGTCAGAACACAGGAGA 180
Db	1532 TGTGGTGAACAACTGAAAAATTTGGAAACCCCTGTGACCGCTGCTGTCAGAACACAGGAGA 1591	607 TGTGGTGAACAACTGAAAAATTTGGAAACCCCTGTGACCGCTGCTGTCAGAACACAGGAGA 666
Qy	181 CACTTCCCAATGCTTTTGT 204	181 CACTTCCCAATGCTTTTGT 204
Db	1592 CACTTCCCAATGCTTTTGT 1615	667 CACTTCCCAATGCTTTTGT 690
RESULT 9		
AF183429		
LOCUS	1491 bp mRNA linear ROD 16-JUL-2002	E31042 1659 bp DNA linear PAT 18-JUN-2001
DEFINITION	Rattus norvegicus inhibitor of apoptosis protein 3 mRNA, complete cds.	Method for screening substance inhibiting binding to XIAP.
ACCESSION	AF183429	E31042
VERSION	AF183429.1	E31042.1
KEYWORDS	GI:10765280	GI:13017307
SOURCE	Norway rat.	JP 1999326328-A/2.
ORGANISM	Rattus norvegicus	unidentified.
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	unclassified.
		1 (bases 1 to 1659)
		Kunihiro, M.
		Method for screening substance inhibiting binding to XIAP
		Patent: JP 1999326328-A 2 26-NOV-1999;
		KUNIHIRO MATSUMOTO
		OS Unidentified

PN JP 1999326328-A/2
 PD 26-NOV-1999
 PF 13-MAY-1998 JP 1998130378
 PR KUNITHIRO MATSUMOTO
 PI G01N33/536, G01N33/00, A61K38/00, A61K38/00, A61K38/22, A61K39/395,
 PC G01N33/536, G01N33/00, A61K45/00, C07K7/06, C07K14/47, PC
 PC A61K37/02, PC A61K37/02, C12N15/09, C12P21/08, A61K37/02,
 PC A61K37/02, A61K37/24, C12N15/00
 CC Strandedness: Double;
 CC Topology: Linear;
 FH Key Location/Qualifiers
 FT CDS 82..1572.

FEATURES

source

BASE COUNT 519 a 296 c 385 g 459 t

ORIGIN

Query Match 84.3%; Score 172; DB 6; Length 1659;
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 Db 568 GAAGAAGCTAGATTAAAGTCTTTTCAGAACTGGCGGACTATGCTCAATTTTAAACCCCGAGA 627
 QY 61 GAGTTAGTCTAGTGGCTCTACTACACAGGCGCTGATGATCAAGTGCATGCTTTTGT 120
 Db 628 GAGTTAGTCTAGTGGCTCTACTACACAGGCTGATGATCAAGTGCATGCTTTTGT 687
 QY 121 TGTGGGAAACCTGAAATTTGGAACTTGGTGTGATCGTGGCTGTCAGACAGGAGA 180
 Db 688 TGTGGTGAACCTGAAATTTGGAACTTGGTGTGATCGTGGCTGTCAGACAGGAGA 747
 QY 181 CACTTTCCCAATGCTTTTGT 204
 Db 748 CACTTTCCCAATGCTTTTGT 771

RESULT 11

HSU32974

LOCUS

DEFINITION Human IAP-like protein ILP mRNA, complete cds. PRI 12-JUN-1996

ACCESSION

U32974

VERSION

U32974.1

KEYWORDS

apoptosis; ring finger; zinc finger.

SOURCE

Homo sapiens

ORGANISM

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1

Duckett,C.S., Nava,V.E., Gedrich,R.W., Clem,R.J., Van Dongen,J.L.,
 Glifflin,M.C., Shields,H., Hardwick,J.M. and Thompson,C.B.
 A conserved family of cellular genes related to the baculovirus iap
 gene and encoding apoptosis inhibitors
 EMBO J. 15 (11), 2685-2694 (1996)

MEDLINE

96256286

PUBMED

8654366

REFERENCE

2

Duckett,C.S. and Thompson,C.B.
 Direct Submission
 Submitted (01-AUG-1995) Colin Duckett, Howard Hughes Medical
 Institute, The University of Chicago, 924 East 57th Street,
 Chicago, IL 60637, USA

AUTHORS

TITLE

JOURNAL

JOURNAL

FEATURES

source

1..1659

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 QY 61 GAGTTAGTCTAGTGGCTCTACTACACAGGCGCTGATGATCAAGTGCATGCTTTTGT 120
 Db 628 GAGTTAGTCTAGTGGCTCTACTACACAGGCTGATGATCAAGTGCATGCTTTTGT 687
 QY 121 TGTGGGAAACCTGAAATTTGGAACTTGGTGTGATCGTGGCTGTCAGACAGGAGA 180
 Db 688 TGTGGTGAACCTGAAATTTGGAACTTGGTGTGATCGTGGCTGTCAGACAGGAGA 747
 QY 181 CACTTTCCCAATGCTTTTGT 204
 Db 748 CACTTTCCCAATGCTTTTGT 771

RESULT 12

BC032729

LOCUS

DEFINITION

Homo sapiens, baculoviral IAP repeat-containing 4, clone MGC:45369

IMAGE:5532247, mRNA, complete cds.

ACCESSION

BC032729

VERSION

BC032729.1

KEYWORDS

MGC.

SOURCE

human.

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE

1

(bases 1 to 2086)
 Strausberg,R.
 Direct Submission
 Submitted (06-JUN-2002) National Institutes of Health, Mammalian
 Gene Collection (MGC), Cancer Genomics Office, National Cancer
 Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
 USA
 NIH-MGC Project URL: http://mgc.nci.nih.gov
 Contact: MGC help desk
 Email: cgabs-remail.nih.gov
 Tissue Procurement: ATCC

AUTHORS

TITLE

JOURNAL

REMARK

COMMENT

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run On: April 15, 2003, 19:38:17 ; Search time 136,354 Seconds
(without alignments)
3369,223 Million cell updates/sec

Title: US-09-654-743-50
Perfect score: 204
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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 1125999159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Result No.	Score	Query Match	Length	DB ID	Description
1	204	100.0	2100	18 AAT70839	Mouse apoptosis in
2	204	100.0	2100	24 ABK3872	Mouse cDNA encodin
3	204	100.0	2691	19 AAV55041	Murine XIAP coding
4	202	99.2	1988	18 AAT72710	Mouse inhibitor of
5	172	84.3	1659	21 AAZ48862	Human XIAP coding
6	172	84.3	2540	21 AAT70836	Human apoptosis in
7	172	84.3	2540	21 AAA64901	Human X-linked inh
8	172	84.3	2540	24 ABK93869	Human cDNA encodin
9	172	84.3	3000	24 ABK93875	Human cDNA encodin

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

10	172	84.3	5232	19 AAV55038	Human XIAP coding
11	161	78.9	2404	24 AAK99405	DNA of APP related
12	156	76.5	1758	24 ABK14677	Human Inhibitor of
13	154.4	75.7	1559	24 ABK13197	Human testes speci
14	154.4	75.7	1758	24 ABK14678	Human inhibitor of
15	154.4	75.7	4993	22 AAD03581	Human IAP-like pro
16	120.8	59.2	7990	24 ABL54307	Chemically treated
17	120.8	59.2	7990	24 ABL32158	Human immune syste
18	103.8	50.9	7990	24 ABL54308	Chemically treated
19	103.8	50.9	7990	24 ABL32159	Human immune syste
20	81.4	39.9	2601	18 AAT61591	Human c-IAP2. Hom
21	81.4	39.9	2666	18 AAT70837	Human apoptosis in
22	81.4	39.9	2676	24 ABK93870	Human cDNA encodin
23	81.4	39.9	3076	18 AAT72712	Human inhibitor of
24	81.4	39.9	3076	20 AAZ41005	Human cellular inh
25	81.4	39.9	3076	20 AAZ22096	Human cellular inh
26	81.4	39.9	3076	24 ABL62746	Breast cancer rela
27	81.4	39.9	3076	24 ABL66325	Lung cancer relate
28	81.4	39.9	3734	22 AAC90972	Human API2-MIT chi
29	81.4	39.9	3734	24 ABK52387	DNA encoding cysti
30	81.4	39.9	6669	19 AAV55039	Human XIAP-1 codin
31	81.4	39.9	6669	24 ABK93876	Human cDNA encodin
32	72.8	35.7	2862	18 AAT61592	Murine c-IAP. Mus
33	72.8	35.7	3151	19 AAV55043	Murine XIAP-2 codi
34	71.8	35.2	2291	22 AAS06025	Angiotensin conver
35	71.8	35.2	2580	18 AAT70838	Human apoptosis in
36	71.8	35.2	2580	24 ABK93871	Human cDNA encodin
37	71.8	35.2	2580	18 AAT61590	Human c-IAP1. Hom
38	71.8	35.2	3532	18 AAT72711	Human inhibitor of
39	71.8	35.2	3532	20 AAZ22143	Human cellular inh
40	71.8	35.2	3532	24 ABK96857	Gene #3355 used to
41	71.8	35.2	3732	19 AAV55040	Human XIAP-2 codin
42	71.2	34.9	2416	18 AAT70841	Mouse apoptosis in
43	71.2	34.9	2416	24 ABK93874	Mouse cDNA encodin
44	70.2	34.4	1435	17 AAT43709	Human inhibitor of
45	63	30.9	2474	18 AAT70840	Mouse apoptosis in

ALIGNMENTS

RESULT 1

AA70839	standard; cDNA; 2100 BP.
XX	AA70839;
XX	02-SEP-1997 (first entry)
DE	Mouse apoptosis inhibitor m-xiap cDNA.
XX	Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
KW	M-XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;
KW	Ischaemia; myocardial infarction; stroke;
KW	Reperfusion injury; toxin-induced liver disease; gene therapy;
KW	diagnosis; ds.
OS	Mus sp.
PH	Key
FT	CDS
FT	Location/Qualifiers
FT	127..1617
FT	/*tag= a
XX	WO9706255-A2.
PN	20-FEB-1997.
XX	05-AUG-1996; 96WO-IB01022.
XX	22-DEC-1995; 95US-0576956.
PR	04-AUG-1995; 95US-0511485.
XX	(UYOT-) UNIV OTTAWA.

XX PI Baird S, Korneluk RG, Liston P, Mackenzie AE;
 XX WPI; 1997-154262/14.
 DR P-PSDB; AAW19584.
 XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
 PT of susceptibility to apoptotic disease
 XX Claim 11; Page 78-79; 219pp; English.
 XX Human XIAP, hiap-1 and hiap-2 genes, and murine XIAP, hiap-1 and
 CC hiap-2 genes (AA70836-41) respectively code for a new class of
 CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis
 CC (IAP). The murine XIAP gene (for X-linked IAP gene) sequence was
 CC constructed from 12 overlapping clones isolated from a mouse
 CC embryo lambda-gt11 cDNA library and from a mouse FIX II genomic
 CC library using human XIAP cDNA as probe. IAP nucleic acids can be
 CC used to express IAP polypeptides in cells and animals to inhibit
 CC apoptosis, and as primers and probes to identify and isolate
 CC additional IAP genes, as well as in methods for treating diseases
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).
 XX Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;
 SQ Query Match 100.0%; Score 204; DB 18; Length 2100;
 Best Local Similarity 100.0%; Pred. No. 1.1e-61;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCAATTCAGAACTGGCGGACTGCTCATTTAAACCCCGAGA 60
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QY 61 GAGTTAGTCTAGTGGCTCTACTACAGAGGCTGATGATCAAGTCAATGCTTTTGT 120
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QY 121 TGTGGGGAAACTGAAAAATTGGAAACCCCTGTGATGCTGCTGTCAGAACACAGGAGA 180
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QY 181 CACTTTCCCAATGCTTTTGT 204
 Db 793 CACTTTCCCAATGCTTTTGT 816

RESULT 2
 ABK93872
 ID ABK93872 standard; cDNA; 2100 BP.
 XX AC ABK93872;
 XX 26-AUG-2002 (first entry)
 XX Mouse cDNA encoding inhibitor of apoptosis, XIAP.

XX Mouse; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
 KW cytosolic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
 KW pancreatic cancer; embryonic development; viral pathogenesis;
 KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
 KW lupus erythematosus; herpes virus infection; pox virus infection;
 KW adenovirus infection; proliferative disease.
 XX Mus sp.
 XX WO200226968-A2.
 XX 04-APR-2002.
 XX 27-SEP-2001; 2001WO-CA01379.
 XX 28-SEP-2000; 2000US-0672717.

XX (UYOT-) UNIV OTTAWA.
 PA (AEGE-) AEGERA THERAPEUTICS INC.
 XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
 XX WPI; 2002-479562/51.
 DR P-PSDB; ABG65666.
 XX Novel antisense inhibitor of apoptosis nucleic acid useful for
 PT enhancing apoptosis in a cell, for treating cancer and other
 PT proliferative diseases
 XX Disclosure; Fig 4; 135pp; English.
 XX The invention relates to an inhibitor of apoptosis (IAP) antisense
 CC nucleic acid (1) that inhibits IAP biological activity, regardless of
 CC length of the antisense nucleic acid, the IAP proteins may be mouse
 CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
 CC composition comprising a mammalian IAP antisense molecule and a method of
 CC enhancing apoptosis in a cell, comprising administering a negative
 CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
 CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
 CC mammal diagnosed with a proliferative disease. The method is useful for
 CC treating a patient diagnosed with a proliferative disease like cancer.
 CC The IAP antisense molecule is useful to treat, ameliorate, improve,
 CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
 CC adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or
 CC conditions where apoptosis is involved or implicated (e.g. embryonic
 CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
 CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
 CC virus, pox virus and adenovirus). The present sequence is a mouse IAP
 CC cDNA sequence.
 XX Sequence 2100 BP; 615 A; 417 C; 482 G; 586 T; 0 other;
 SQ Query Match 100.0%; Score 204; DB 24; Length 2100;
 Best Local Similarity 100.0%; Pred. No. 1.1e-61;
 Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 Db 613 GAAGAAGCCAGATTGAAGTCAATTCAGAACTGGCGGACTGCTCATTTAAACCCCGAGA 672

QY 61 GAGTTAGTCTAGTGGCTCTACTACAGAGGCTGATGATCAAGTCAATGCTTTTGT 120
 Db 673 GAGTTAGTCTAGTGGCTCTACTACAGAGGCTGATGATCAAGTCAATGCTTTTGT 732

QY 121 TGTGGGGAAACTGAAAAATTGGAAACCCCTGTGATGCTGCTGTCAGAACACAGGAGA 180
 Db 733 TGTGGGGAAACTGAAAAATTGGAAACCCCTGTGATGCTGCTGTCAGAACACAGGAGA 792

QY 181 CACTTTCCCAATGCTTTTGT 204
 Db 793 CACTTTCCCAATGCTTTTGT 816

RESULT 3
 AAV55041
 ID AAV55041 standard; cDNA; 2691 BP.
 XX AC AAV55041;
 XX 13-NOV-1998 (first entry)
 XX Murine XIAP coding sequence.
 XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
 KW proliferative disease; IAP; therapy; cancer; mouse; XIAP protein; ss.
 XX Mus sp.
 XX FH Key Location/Qualifiers

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FT CDS      672..2162
FT          /*tag= a
FT          /product= XIAP
XX WO9835693-A2.
XX 20-AUG-1998.
XX
XX 13-FEB-1998; 98WO-IB00781.
XX 13-FEB-1997; 97US-0800929.
XX (UYOT-1) UNIV OTTAWA.
XX
XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
XX Tsang B;
XX
XX WPI; 1998-467164/40.
XX P-PSDB; AAW69297.
XX
XX Inducing apoptosis in proliferative mammalian cells with inhibitor
XX of IAP or NAIP polypeptide - also methods for prognosis based on
XX presence of IAP and NAIP, specifically applied to cancers involving
XX p53 mutations
XX
XX Claim 13; Fig 4; 147pp; English.
XX
XX This sequence encodes the mouse XIAP protein, which is a inhibitor of
XX apoptosis protein (IAP), and can be used in the method of the invention.
XX The method is for enhancing apoptosis in cells from a mammal with
XX proliferative disease by treatment with a compound that inhibits
XX biological activity of an IAP or NAIP polypeptide. The inhibitory
XX compounds are used to treat proliferative diseases, specially cancers of
XX ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
XX liver nasopharynx, thyroid, central nervous system, prostate, colon,
XX rectum, cervix or endometrium, particularly to increase their sensitivity
XX to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
XX detected in many cancers and are associated with poor prognosis,
XX resistance to chemotherapeutic agents and mutations in p53 (it is
XX suggested that wild-type p53 suppresses transcription of the IAP or NAIP
XX genes). Transgenic animals are used for testing the effects of antisense
XX oligonucleotides and for screening for the inhibitors.
XX
XX Sequence 2691 BP; 819 A; 479 C; 562 G; 831 T; 0 other;
XX
XX Query Match      100.0%; Score 204; DB 19; Length 2691;
XX Best Local Similarity 100.0%; Pred. No. 1.2e-61;
XX Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX QY 1 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCGGAGTATGCTCATTTAACCCCCAGA 60
XX |||||||
XX DB 1158 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCGGAGTATGCTCATTTAACCCCCAGA 1217
XX |||||||
XX QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120
XX |||||||
XX DB 1218 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 1277
XX |||||||
XX QY 121 TGTGGGGGAAAACACTGAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGAACACAGGAGA 180
XX |||||||
XX DB 1278 TGTGGGGGAAAACACTGAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGAACACAGGAGA 1337
XX |||||||
XX QY 181 CACTTTCCCAATTGCTTTTGT 204
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XX DB 1338 CACTTTCCCAATTGCTTTTGT 1361
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XX
XX RESULT 4
XX AAT72710
XX ID AAT72710 standard; DNA; 1988 BP.
XX AC AAT72710;
XX XX
XX DT 16-SEP-1997 (first entry)

```

```

XX Mouse inhibitor of apoptosis protein homologue MIHA DNA.
XX
XX Inhibitor of apoptosis protein; IAP; mammalian IAP homologue; MIHA;
XX KW degenerative disease; infectious disease; autoimmune disease;
XX KW cancer; gene therapy; diagnosis; ss.
XX
XX OS Mus musculus.
XX
XX FH Key Location/Qualifiers
XX FT CDS 212..1702
XX FT /*tag= a
XX
XX PN WO9723501-A1.
XX PD 03-JUL-1997.
XX
XX PF 20-DEC-1996; 96WO-AU00827.
XX
XX PR 22-DEC-1995; 95AU-0007275.
XX
XX PA (AMRA-) AMRAD OPERATIONS PTY LTD.
XX
XX PI Vaux DL;
XX
XX WPI; 1997-350966/32.
XX P-PSDB; AAW19745.
XX
XX Isolated protein homologues of viral inhibitors of apoptosis - used
XX to modulate apoptosis for treatment of degenerative, infectious or
XX autoimmune diseases and cancer
XX
XX Claim 24; Page 44-47; 136pp; English.
XX
XX An isolated nucleic acid molecule (AAT72710) codes for mammalian IAP
XX homologue A (MIHA) (AAW19745), a murine homologue of baculovirus
XX inhibitor of apoptosis protein (IAP). It was isolated from a mouse
XX liver cDNA library on the basis of homology to Orgyia pseudotsugata
XX polyhedrosis virus IAP BIR and RING finger amino acid motifs.
XX Animal IAP homologue nucleic acids (see also AAT72711-17) can be used
XX to produce polypeptides useful in methods for modulating apoptosis
XX in animal cells, specifically for treatment, by inhibition, of
XX degenerative and infectious disease or, by promotion, of cancer and
XX autoimmune disease, and can be used for gene therapy of these
XX diseases.
XX
XX Sequence 1988 BP; 605 A; 367 C; 459 G; 557 T; 0 other;
XX
XX Query Match      99.2%; Score 202.4; DB 18; Length 1988;
XX Best Local Similarity 99.5%; Pred. No. 4e-61;
XX Matches 203; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
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XX DB 698 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCGGAGTATGCTCATTTAACCCCCAGA 757
XX |||||||
XX QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120
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XX DB 758 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 817
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XX DB 818 TGTGGGGGAAAACACTGAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGAACACAGGAGA 877
XX |||||||
XX QY 181 CACTTTCCCAATTGCTTTTGT 204
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XX DB 878 CACTTTCCCAATTGCTTTTGT 901
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XX
XX RESULT 5
XX AA248862
XX ID AA248862 standard; cDNA; 1659 BP.
XX XX

```


AC AA248862;
 XX 24-MAR-2000 (first entry)
 DT XX Human XIAP coding sequence.
 DE XX
 XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
 KW transforming growth factor-beta activated kinase 1; monocyte migration;
 KW TAK1 binding protein 1; extracellular matrix protein production;
 KW cell growth inhibitor; beta-amyloid protein deposition;
 KW immunosuppression; transforming growth factor-beta; ds.
 XX OS Homo sapiens.
 XX JPL1326328-A.
 XX 26-NOV-1999.
 XX 13-MAY-1998; 98JP-0130378.
 XX 13-MAY-1998; 98JP-0130378.
 XX (MATS/) MATSUMOTO K.
 XX WPI; 2000-078337/07.
 XX P-PSDB; AAY59451.
 PT Screening a substance which inhibits combination of the X-linked
 PT inhibitor of apoptosis protein -
 XX Disclosure; Page 28-30; 43pp; Japanese.
 XX This sequence encodes the human XIAP protein.
 CC The invention relates to a method for screening a substance inhibiting
 CC the formation of a complex between XIAP and TAB1, in which X-linked
 CC inhibitor of apoptosis protein (XIAP), transforming growth factor-beta
 CC activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be
 CC tested are contacted with each other and then the presence or formation
 CC of a complex between XIAP and TAB1 is detected. The substance can be used
 CC as a drug for extracellular matrix protein production enhancement, cell
 CC growth inhibition, monocyte migration, physiologically active substance
 CC induction, immunosuppression, and beta-amyloid protein deposition. A
 CC substance inhibiting the formation of a complex between TAB1 and XIAP as
 CC well as between XIAP and TGF-beta (Transforming growth factor-beta) type
 CC I and/or type II receptor is useful as a drug.
 XX Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;
 SQ
 Query Match 84.3%; Score 172; DB 21; Length 1659;
 Best Local Similarity 90.2%; Pred. No. 2.1e-50;
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 GAAGAAGCCAGATTGAAGTCAATTTTCAGAACTGGCGGACACTATGCTCATTTAACCCCCAGA 60
 DB 568 GAAGAAGCTAGATTAAAGTCTCTTCAGAACTGGCGGACACTATGCTCACCTAACCCCAAGA 627
 QY 61 GAGTAGTCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 120
 DB 628 GAGTTAGCAAGTGTGGACACTACTACACAGGTATTGTTGACCAAGTGCACTGCTTTTGT 687
 QY 121 TGTGGGGAAACCTGAAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGACACAGAGA 180
 DB 688 TGTGGTGGAAACCTGAAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGACACAGCGGA 747
 QY 181 CACTTTCCCAATTCCTTTTGT 204
 DB 748 CACTTTCCCAATTCCTTTTGT 771
 RESULT 6
 AAT70836
 ID AAT70836 standard; cDNA; 2540 BP.
 XX

AC AAT70836;
 XX 02-SEP-1997 (first entry)
 DT XX Human apoptosis inhibitor xiap cDNA.
 DE XX
 XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
 KW XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;
 KW ischaemia; myocardial infarction; stroke;
 KW reperfusion injury; toxin-induced liver disease; gene therapy;
 KW diagnosis; ds.
 XX OS Homo sapiens.
 XX Key Location/Qualifiers
 FT CDS 34..1527
 FT /*tag= a
 XX WC9706255-A2.
 XX 20-FEB-1997.
 XX 05-AUG-1996; 96WO-1B01022.
 XX 22-DEC-1995; 95US-0576956.
 XX 04-AUG-1995; 95US-0511485.
 XX (UYOT-) UNIV OTTAWA.
 XX Baird S, Korneluk RG, Liston P, Mackenzie AE;
 PI WPI; 1997-154262/14.
 DR P-PSDB; AAW19581.
 DR Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
 PT of susceptibility to apoptotic disease
 XX Claim 12: Page 67-68; 219pp; English.
 XX Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and
 CC hiap-2 genes (AAT70836-41) respectively code for a new class of
 CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis
 CC (IAP). The xiap gene (for X-linked IAP gene) was isolated from a
 CC human foetal brain ZapII cDNA library using an X-linked sequence
 CC tag site that shows strong homology with the conserved ring zinc
 CC finger domain of baculovirus CpiAP and OpiAP genes. The gene was
 CC assigned to chromosome Xq25 by FISH. IAP nucleic acids can be used
 CC to express IAP polypeptides in cells and animals to inhibit
 CC apoptosis, and as primers and probes to identify and isolate
 CC additional IAP genes, as well as in methods for treating diseases
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).
 XX Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 1 other;
 SQ
 Query Match 84.3%; Score 172; DB 18; Length 2540;
 Best Local Similarity 90.2%; Pred. No. 2.5e-50;
 Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;
 QY 1 GAAGAAGCCAGATTGAAGTCAATTTTCAGAACTGGCGGACACTATGCTCATTTAACCCCCAGA 60
 DB 520 GAAGAAGCTAGATTAAAGTCTCTTCAGAACTGGCGGACACTATGCTCACCTAACCCCAAGA 579
 QY 61 GAGTAGTCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 120
 DB 580 GAGTTAGCAAGTGTGGACACTACTACACAGGTATTGTTGACCAAGTGCACTGCTTTTGT 639
 QY 121 TGTGGGGAAACCTGAAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGACACAGAGA 180
 DB 640 TGTGGTGGAAACCTGAAAATTTGGAAACCTGTGATCGTGCCTGGTGCAGACACAGCGGA 699
 QY 181 CACTTTCCCAATTCCTTTTGT 204
 XX

Db	540	TGTGGTGGAAATCGAAAATGGGACCTTGTGATCTGCTGCTCAGACACAGCGGA	699
QY	181	CACTTTCCCAATTGCTTTTTTGTT	204
Db	700	CACTTTCCCTAATTGCTTCTTGTT	723
RESULT 8			
ABK93869			
ID	ABK93869	standard; cDNA; 2540 BP.	
XX	AC	ABK93869;	
XX	XX	26-AUG-2002 (first entry)	
XX	XX	Human cDNA encoding inhibitor of apoptosis, XIAP #1.	
XX	XX	Human; ss: gene; antisense: inhibitor of apoptosis; HIAP1; HIAP2; XIAP;	
KW	KW	cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;	
KW	KW	pancreatic cancer; embryonic development; viral pathogenesis;	
KW	KW	autoimmune disorder; neurodegenerative disease; multiple sclerosis;	
KW	KW	lupus erythematosus; herpes virus infection; pox virus infection;	
KW	KW	adenovirus infection; proliferative disease.	
XX	XX		
OS	OS	Homo sapiens.	
XX	XX	W0200226968-A2.	
PN	PN	04-APR-2002.	
PD	PD	27-SEP-2001; 2001WO-CA01379.	
PF	PF	28-SEP-2000; 2000US-0672717.	
XX	XX	(UYOT-) UNIV OTTAWA.	
PA	PA	(ABGE-) ABGERA THERAPEUTICS INC.	
XX	XX	Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;	
PI	PI	WPI; 2002-479562/51.	
XX	XX	P-PSDB; ABG65663.	
DR	DR	Novel antisense inhibitor of apoptosis nucleic acid useful for	
XX	XX	enhancing apoptosis in a cell, for treating cancer and other	
PT	PT	proliferative diseases	
PT	PT	Disclosure; Fig 1; 135pp; English.	
XX	XX	The invention relates to an inhibitor of apoptosis (IAP) antisense	
CC	CC	nucleic acid (I) that inhibits IAP biological activity, regardless of	
CC	CC	length of the antisense nucleic acid, the IAP proteins may be mouse	
CC	CC	or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical	
CC	CC	composition comprising a mammalian IAP antisense molecule and a method of	
CC	CC	enhancing apoptosis in a cell, comprising administering a negative	
CC	CC	regulator of the IAP anti-apoptotic pathway to the cell. The IAP	
CC	CC	antisense inhibitor is useful for enhancing apoptosis in a cell in a	
CC	CC	mammal diagnosed with a proliferative disease. The method is useful for	
CC	CC	treating a patient diagnosed with a proliferative disease like cancer.	
CC	CC	The IAP antisense molecule is useful to treat, ameliorate, improve,	
CC	CC	sustain or prevent proliferative diseases (e.g. ovarian cancer,	
CC	CC	adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or	
CC	CC	conditions where apoptosis is involved or implicated (e.g. embryonic	
CC	CC	development, viral pathogenesis, autoimmune disorders, neurodegenerative	
CC	CC	diseases, multiple sclerosis, lupus erythematosus) and infection by herpes	
CC	CC	virus, pox virus and adenovirus). The present sequence is a human IAP	
CC	CC	cDNA sequence.	
XX	XX	Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;	
SQ	XX		
Query Match		84.3%; Score 172; DB 24; Length 2540;	
Best Local Similarity		90.2%; Pred. No. 2.5e-50;	
Matches 184; Conservative		0; Mismatches 20; Indels 0; Gaps 0	

XX 18-JUL-2001; 2001WO-EP08287.
 XX PF
 XX PR
 XX 28-JUL-2000; 2000EP-0116452.
 XX PA
 XX (MERE) MERCK PATENT GMBH.
 XX PI
 XX Hentsch B;
 XX DR
 XX WPI; 2002-188741/24.
 XX DR P-PSDB; AAU75747.
 XX PT
 XX New inhibitor of apoptosis proteins and polynucleotides useful in
 PT vaccines for inducing an immune response against hyperproliferative
 PT diseases e.g. cancer
 XX
 XX Claim 5; Page 33-35; 41pp; English.
 XX
 CC This invention relates to the nucleic acid and protein sequences of a
 CC novel inhibitor apoptosis protein (IAPL7) polypeptide. These sequences
 CC have homology to the IAP (inhibitors of apoptosis) gene family which
 CC are thought to inhibit proteins by regulating the anti-apoptotic
 CC activity of the v-rel and NF-kappaB family of transcription factors.
 CC The gene for IAPL7 is located on human chromosome 19. The nucleic acids
 CC of the invention are useful for screening to identify compounds that
 CC stimulate or inhibit the function or level of IAPL7, where the
 CC identified compounds are useful for treating hyper-proliferative
 CC diseases such as cancer. The protein sequences may also be used to
 CC identify membrane bound or soluble receptors of IAPL7 by standard
 CC receptor binding techniques. Nucleic acids encoding IAPL7, may be used
 CC as hybridisation probes for cDNA and genomic DNA, or as primers for
 CC nucleic acid amplification reaction and the primers and probes may also
 CC be used to isolate full-length cDNAs and genomic clones encoding IAPL7.
 CC The nucleic acid sequences are useful as diagnostic reagents for
 CC diagnosing a disease or a susceptibility to a disease by detecting
 CC mutations in the associated gene. The nucleic acid sequence is useful
 CC for chromosome localisation and tissue expression studies and is also
 CC useful for producing transgenic animals. The IAPL7 protein sequence may
 CC also be used to generate an anti-IAPL7 antibody which is useful in
 CC screening methods for detecting the effect of added compounds on the
 CC production of mRNA and protein in cells. The sequences of the invention
 CC are also useful as vaccines for inducing an immunological response in a
 CC mammal. The present sequence represents the cDNA encoding the human
 CC inhibitor of apoptosis 7 (IAP7) protein of the invention.
 XX
 SQ Sequence 1758 BP; 488 A; 371 C; 470 G; 429 T; 0 other;
 Query Match 76.5%; Score 156; DB 24; Length 1758;
 Best Local Similarity 85.3%; Pred. No. 9.9e-45;
 Matches 174; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
 QY 1 GAAGAAGCCAGATTGAAGTTCAGAACTGGCGGACTATGCTCATTTAAACCCCGAGA 60
 DB 673 GAAGAAGCTAGATTACAGTCTTTTCAGAACTGGCGGACTATGCTCATTTAAACCCCGAGA 732
 QY 61 GAGTACCTAGTCTGGCTCTTACTACACAGGGGCTGATGATCAAGTCAATGCTTTGT 120
 DB 733 GAGCTGGCCAGTCTGGCTGTACTACACAGGCACTGATGACCAAGTSCAGTCTCTGT 792
 QY 121 TGTGGGGGAACAAATGAAATTTGGACACCTGTGATCGTGGTGGTCAACACAGGAGA 180
 DB 793 TGTGGCGGAACAACTGAAACCTGGGAACCTGGTGTGCTGCTGGTCAACACAGGAGA 852
 QY 181 CACTTCCCAATCTCTTTTGT 204
 DB 853 CATTTCCTAATCTCTCTTATT 876

RESULT 13

ABK13197

ID ABK13197 standard; DNA; 1559 BP.

XX AC ABK13197;

XX 23-APR-2002 (first entry)
 XX DE
 XX Human testes specific inhibitor of apoptosis (TIAP) gene.
 XX KW
 KW TIAP; apoptosis; testes specific inhibitor of apoptosis; gene;
 KW human; ds; apoptotic; cytostatic; anti-infertility; contraceptive;
 KW chromosome 12q22-23; transgenic animal; antibody; immunogen;
 KW testicular cell; testicular cancer; cancer; male infertility;
 KW male birth control; XIAP.
 XX OS
 OS Homo sapiens.
 XX FH
 FH Key Location/Qualifiers
 FT CDS 791..1501
 FT /tag- a
 FT /product- "TIAP protein"
 XX
 XX US6331412-B1.
 XX 18-DEC-2001.
 XX PF 29-JAN-1999; 99US-0239867.
 XX PR 29-JAN-1998; 98US-073001P.
 XX (UYOT-) UNIV OTTAWA.
 XX Korneluk RG, Lagace M;
 XX WPI; 2002-105275/14.
 XX P-PSDB; AAU75066.
 XX Nucleic acids encoding a testis specific apoptosis inhibitor protein
 PT (TIAP) useful for treating testicular cancers, cancers in
 PT non-testicular tissues, male infertility, and for achieving male birth
 PT control
 XX Claim 2; Fig 4A; 29pp; English.
 XX
 CC This invention relates to a novel isolated nucleic acid molecule
 CC encoding a TIAP polypeptide (testes-specific inhibitor of apoptosis)
 CC protein. This gene is a homologue of the X-linked XIAP gene and is
 CC located on chromosome 12q22-23. The nucleotide and protein sequences of
 CC the invention and vectors containing these sequences may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate TIAP expression. Additionally, the nucleotide sequence may
 CC be used to express the TIAP protein by recombinant methods. Conversely,
 CC antisense nucleic acid molecules may be administered to down-regulate
 CC TIAP expression. The nucleotide sequence, may also be used to design DNA
 CC probes for diagnostic assays (e.g. polymerase chain reactions (PCR)) to
 CC detect and quantitate the presence of similar nucleic acid sequences in
 CC samples, to identify patients who may be in need of restorative therapy.
 CC Through the production of transgenic animals and cells, the sequences
 CC may also be used to study the expression and function of TIAP proteins
 CC and their role in metabolism. The TIAP polypeptides may be used to
 CC produce antibodies against TIAP and maybe used to identify modulators
 CC (agonists and antagonists) of TIAP expression and activity. An anti-TIAP
 CC antibody or antagonist may also be used to down-regulate TIAP expression
 CC and activity. The reagents may be used in this way for the treatment of
 CC excessive or insufficient apoptosis, particularly in testicular cells.
 CC In particular they are useful in diagnosing and treating testicular
 CC cancers, cancers in non-testicular tissues, male infertility, and for
 CC achieving male birth control. The present sequence represents the
 CC human TIAP gene sequence of the invention.
 XX
 SQ Sequence 1559 BP; 465 A; 309 C; 396 G; 387 T; 2 other;
 Query Match 75.7%; Score 154.4; DB 24; Length 1559;
 Best Local Similarity 84.8%; Pred. No. 3.5e-44;
 Matches 173; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
 QY 1 GAAGAAGCCAGATTGAAGTTCAGAACTGGCGGACTATGCTCATTTAAACCCCGAGA 60


```

XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.
XX PI Duckett C, Mir SS;
XX PI WPI: 2001-258135/26.
XX DR P-PSDB: AAE00365.
XX PT
XX PT Inhibitors of apoptosis proteins designated ILP-2 and ILP-3 with
XX PT transforming growth factor beta receptor modulating activity, and the
XX PT nucleic acids that encode them, useful for treating, e.g. diabetes and
XX PT multiple sclerosis -
XX PS
XX PS Claim 18: Page 94-98; 108pp; English.
XX PS
XX PS The present sequence is a human inhibitor of apoptosis (IAP)-like protein-2
XX PS (ILP-2) cDNA. The ILP-2 gene is located on chromosome 19q13.3-q13.4.
XX PS ILP-2 comprises a single amino-terminal domain known as baculovirus iap
XX PS repeat (BIR), followed by a spacer region and a carboxy-terminal ring
XX PS finger domain. It interacts with transforming growth factor beta
XX PS receptor (TGFbetaR) and modulates TGFbetaR activity. It also potentially
XX PS inhibits apoptosis induced by overexpression of bax or by Caspase-9 and
XX PS Apaf-1. It also activates c-Jun N-terminal kinase (JNK) activity. ILP-2
XX PS is used in the area of genetic testing for predisposition to diseases,
XX PS such as cone-rod retinal dystrophy-2, retinitis pigmentosa,
XX PS glutaricaciduria, T-cell acute lymphoblastic leukemia, colorectal cancer
XX PS and hyperferritinemia-catatract syndrome owing to an ILP-2 deletion or
XX PS mutation. The ILP is also used in the treatment of diseases associated
XX PS with abnormal apoptosis such as cancer, autoimmune diseases, e.g.,
XX PS diabetes and multiple sclerosis and neurodegenerative diseases including
XX PS retinal degeneration. The ILP-2 gene is also used in gene therapy for
XX PS treating patients suffering from ILP-2 gene deletions or mutations.
XX PS
XX PS Sequence 4993 BP; 1526 A; 973 C; 1196 G; 1297 T; 1 other;
XX PS
XX PS Query Match 75.7%; Score 154.4; DB 22; Length 4993;
XX PS Best Local Similarity 84.8%; Pred. No. 5.7e-44;
XX PS Matches 173; Conservative 0; Mismatches 31; Indels 0; Gaps 0;
XX PS
XX PS 1 GAAGAAGCCAGATGAGTCATTTTCAGAACTGGCGGAGCTATGCTCATTTTAACCCCGAGA 60
XX PS 1777 GAAGAAGCTAGATAACTAGTCGTTTTCAGAACTGGCGGAGCTCTGGCCACTTGACCCCGAGA 1836
XX PS
XX PS 61 GAGTTAGCTAGTGTGCGCTCTACTACAGAGGGCTGATGATCAAGTCGAATGCTTTGT 120
XX PS 1837 GAGCTGGCCAGTGTGGGCTCTACTACAGAGCACTGATGACCAAGTCGAGTCTCTGT 1896
XX PS
XX PS 121 TGTGGGGGAAACTGAAAAATTTGGAAACCCCTGTGATCGTGCCTGGTTCAGAACACAGGAGA 180
XX PS 1897 TGTGGCGGAAACTGAAAAACTGGGAACCTGGTGTGTCGCTGGTTCAGAACACAGGAGA 1956
XX PS
XX PS 181 CACTTTCCCAATTCGCTTTTGT 204
XX PS
XX PS 1957 CATTTTCTTAATGCTTCTTTATT 1980

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Search completed: April 15, 2003, 21:45:40
Job time : 139.354 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:16:42 ; Search time 25.6771 Seconds
(without alignments)
2436.494 Million cell updates/sec

Title: US-09-654-743-50
Perfect score: 204
Sequence: 1 gaagaagcagattgaagtc.....ttcccaattgtttttgtt 204

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3: /cgn2_6/ptodata/1/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	204	100.0	2100	2	US-08-511-485-9
2	204	100.0	2691	3	US-09-212-971-9
3	204	100.0	2691	3	US-08-800-929A-9
4	204	100.0	2691	4	US-09-617-053A-9
5	172	84.3	1588	4	US-09-239-867-3
6	172	84.3	2540	2	US-08-511-485-3
7	172	84.3	2540	3	US-09-392-580-1
8	172	84.3	5232	3	US-09-212-971-3
9	172	84.3	5232	3	US-08-800-929A-3
10	172	84.3	5232	4	US-09-617-053A-3
11	154.4	75.7	1559	4	US-09-239-867-1
12	81.4	39.9	2601	4	US-08-569-749-3
13	81.4	39.9	2601	5	PCT-US96-12860-3
14	81.4	39.9	2676	2	US-08-511-485-5
15	81.4	39.9	3076	2	US-09-205-144-1
16	81.4	39.9	6669	3	US-09-212-971-5
17	81.4	39.9	6669	3	US-08-800-929A-5
18	81.4	39.9	6669	4	US-09-617-053A-5
19	72.8	35.7	2862	4	US-08-569-749-13
20	72.8	35.7	2862	5	PCT-US96-12860-13
21	72.8	35.7	3151	3	US-09-212-971-13
22	72.8	35.7	3151	3	US-08-800-929A-13
23	72.8	35.7	3151	4	US-09-617-053A-13
24	71.8	35.2	2580	2	US-08-511-485-7
25	71.8	35.2	2589	4	US-08-569-749-1
26	71.8	35.2	2589	5	PCT-US96-12860-1
27	71.8	35.2	3532	2	US-09-205-204-1

28	71.8	35.2	3732	3	US-09-212-971-7	Sequence 7, Appli
29	71.8	35.2	3732	3	US-08-800-929A-7	Sequence 7, Appli
30	71.8	35.2	3732	4	US-09-617-053A-7	Sequence 7, Appli
31	70.2	34.4	1435	5	PCT-US95-05922A-1	Sequence 1, Appli
32	63	30.9	2676	3	US-09-212-971-11	Sequence 11, Appli
33	63	30.9	2676	3	US-08-800-929A-11	Sequence 11, Appli
34	63	30.9	2676	4	US-09-617-053A-11	Sequence 11, Appli
35	54.2	26.6	5502	3	US-08-836-134-1	Sequence 1, Appli
36	54.2	26.6	5502	4	US-09-493-784-1	Sequence 1, Appli
37	41.2	20.2	711	3	US-09-121-979-3	Sequence 3, Appli
38	41.2	20.2	711	4	US-09-332-319-3	Sequence 3, Appli
39	35.6	17.5	176373	3	US-09-128-155-17	Sequence 17, Appli
40	34.8	17.1	152331	3	US-09-128-155-16	Sequence 16, Appli
41	32.8	16.1	436	2	US-08-824-701A-7	Sequence 7, Appli
42	29.2	14.3	1400	2	US-08-001-078A-2	Sequence 2, Appli
43	29.2	14.3	1400	2	US-08-463-218-2	Sequence 2, Appli
44	29.2	14.3	1400	5	PCT-US94-00253-2	Sequence 2, Appli
45	28.2	13.8	10614	1	US-08-135-511-35	Sequence 35, Appli

ALIGNMENTS

RESULT 1
US-08-511-485-9
; Sequence 9, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511.485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2100 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: both
; TOPOLOGY: both
; MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match 100.0%; Score 204; DB 2; Length 2100;
Best Local Similarity 100.0%; Pred. No. 5.9e-62;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 GAAGAAGCAGATTGAAGTCATTTTCAGAACTGGCGGACTATGCTTAAACCCAGAGA 60
|||||

Db 613 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGGACTATGCTCATTTTAACCCCCAGA 672
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Db 673 GAGTTAGCTAGTGTGGCCCTCTACTACACAGGGGCTGATGATCAAGTGCATCTTTTGT 732
QY 121 TGTGGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTGCCTGGTCAGAACACAGGAGA 180
Db 733 TGTGGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTGCCTGGTCAGAACACAGGAGA 792
QY 181 CACTTTCCCAATGCTTTTGT 204
Db 793 CACTTTCCCAATGCTTTTGT 816

RESULT 2

US-09-212-971-9
; Sequence 9, Application US/09212971B
; Patent No. 6107041
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009002
; CURRENT APPLICATION NUMBER: US/09/212,971B
; EARLIER FILING DATE: 1998-12-16
; EARLIER APPLICATION NUMBER: 60/017,354
; EARLIER FILING DATE: 1996-04-26
; EARLIER APPLICATION NUMBER: 60/030,590
; EARLIER FILING DATE: 1996-11-14
; EARLIER APPLICATION NUMBER: 08/800,929
; EARLIER FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-212-971-9

Query Match 100.0%; Score 204; DB 3; Length 2691;
Best Local Similarity 100.0%; Pred. No. 6.5e-62;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGGACTATGCTCATTTTAACCCCCAGA 60
Db 1158 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGGACTATGCTCATTTTAACCCCCAGA 1217
QY 61 GAGTTAGCTAGTGTGGCCCTCTACTACACAGGGGCTGATGATCAAGTGCATCTTTTGT 120
Db 1218 GAGTTAGCTAGTGTGGCCCTCTACTACACAGGGGCTGATGATCAAGTGCATCTTTTGT 1277
QY 121 TGTGGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTGCCTGGTCAGAACACAGGAGA 180
Db 1278 TGTGGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTGCCTGGTCAGAACACAGGAGA 1337
QY 181 CACTTTCCCAATGCTTTTGT 204
Db 1338 CACTTTCCCAATGCTTTTGT 1361

RESULT 3

US-08-800-929A-9
; Sequence 9, Application US/08800929A
; Patent No. 613437
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G

; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF
; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERA
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Clark & Ebling LLP
; STREET: 176 Federal Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/800,929A
; FILING DATE: 13-FEB-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/030,590
; FILING DATE: 14-NOV-1996
; APPLICATION NUMBER: 60/017,354
; FILING DATE: 26-APR-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Bleker-Brady, Kristina
; REGISTRATION NUMBER:
; REFERENCE/DOCKET NUMBER: 07891/009001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617-428-0200
; TELEFAX: 617-428-7045
; TELEX:
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2691 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
US-08-800-929A-9

Query Match 100.0%; Score 204; DB 3; Length 2691;
Best Local Similarity 100.0%; Pred. No. 6.5e-62;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGGACTATGCTCATTTTAACCCCCAGA 60
Db 1158 GAAGAAGCCAGATTGAAGTCATTTTCAGAACTGGCCGGACTATGCTCATTTTAACCCCCAGA 1217
QY 61 GAGTTAGCTAGTGTGGCCCTCTACTACACAGGGGCTGATGATCAAGTGCATCTTTTGT 120
Db 1218 GAGTTAGCTAGTGTGGCCCTCTACTACACAGGGGCTGATGATCAAGTGCATCTTTTGT 1277
QY 121 TGTGGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTGCCTGGTCAGAACACAGGAGA 180
Db 1278 TGTGGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTGCCTGGTCAGAACACAGGAGA 1337
QY 181 CACTTTCCCAATGCTTTTGT 204
Db 1338 CACTTTCCCAATGCTTTTGT 1361

RESULT 4

US-09-617-053A-9
; Sequence 9, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:

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; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-617-053A-9

Query Match      100.0%; Score 204; DB 4; Length 2691;
Best Local Similarity 100.0%; Pred. No. 6.5e-62;
Matches 204; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATGAGTCAATTTTCAGAACTGGCCGGGCTGATGCTCAATTTACCCCCGAGA 60
DB 1158 GAAGAAGCCAGATGAGTCAATTTTCAGAACTGGCCGGGCTGATGCTCAATTTACCCCCGAGA 1217
QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGAATGCTTTTGT 120
DB 1218 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGAATGCTTTTGT 1277
QY 121 TGTGGGGAAACTGAAAAATTTGGAACTTGTGATCGCTGTCAGAACACAGGAGA 180
DB 1278 TGTGGGGAAACTGAAAAATTTGGAACTTGTGATCGCTGTCAGAACACAGGAGA 1337
QY 181 CACTTTCCCAATGCTTTTGT 204
DB 1338 CACTTTCCCAATGCTTTTGT 1361

RESULT 5
US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-239-867-3

Query Match      84.3%; Score 172; DB 4; Length 1588;
Best Local Similarity 90.2%; Pred. No. 8.7e-51;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATGAGTCAATTTTCAGAACTGGCCGGGCTGATGCTCAATTTACCCCCGAGA 60
DB 520 GAAGAAGCTAGATTAAGTCCCTTTCAGAACTGGCCGGGCTGATGCTCAATTTACCCCAAGA 579
QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGAATGCTTTTGT 120
DB 580 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGAATGCTTTTGT 639
QY 121 TGTGGGGAAACTGAAAAATTTGGAACTTGTGATCGCTGTCAGAACACAGGAGA 180
DB 640 TGTGGGGAAACTGAAAAATTTGGAACTTGTGATCGCTGTCAGAACACAGGAGA 699
QY 181 CACTTTCCCAATGCTTTTGT 204

Query Match      84.3%; Score 172; DB 2; Length 2540;
Best Local Similarity 90.2%; Pred. No. 1e-50;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATGAGTCAATTTTCAGAACTGGCCGGGCTGATGCTCAATTTACCCCCGAGA 60
DB 520 GAAGAAGCTAGATTAAGTCCCTTTCAGAACTGGCCGGGCTGATGCTCAATTTACCCCAAGA 579
QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGAATGCTTTTGT 120
DB 580 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGAATGCTTTTGT 639
QY 121 TGTGGGGAAACTGAAAAATTTGGAACTTGTGATCGCTGTCAGAACACAGGAGA 180
DB 640 TGTGGGGAAACTGAAAAATTTGGAACTTGTGATCGCTGTCAGAACACAGGAGA 699
QY 181 CACTTTCCCAATGCTTTTGT 204
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ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 2676 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: both
MOLECULE TYPE: DNA (genomic)

US-08-511-485-5

Query Match 39.9%; Score 81.4; DB 2; Length 2676;

Best Local Similarity 66.0%; Pred. No. 6e-19;

Matches 134; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 GAAGAAGCCAGATTGAAGTCAATTCAGAACTGGCCGGACTATGCTCATTTAACCCCCAGA 60

Db 693 GAAATGCCAGATTACTTACTTTTCAGACATGGCC---ATTGACTTTTCTGTGCCCAACA 749

QY 61 GAGTTAGCTAGTCTGCTGGCCTCTACTACAGAGGGGCTGATGATCAAGTCAATGCTTTTGT 120

Db 750 GATCTGGCAGCAGCAGGCTTTTACTACATAGGACCTGGAGACAGAGTGGCTTGGCTTGGC 809

QY 121 TGTGGGGAAACTGAAATTTGGGAACCTGTGATCGTCCCTGGTGCAGAACACAGGAGA 180

Db 810 TGTGGTGGAAATTTAGCAATTTGGGAACCGAGAGATGATGCTATGTCAGAACACCTGAGA 859

QY 181 CACTTTCCCAATTCGTTTTTGT 203

Db 870 CATTITCCCAATGCCCATTTAT 892

RESULT 15

US-09-205-144-1

Sequence 1, Application US/09205144

Patent No. 5958771

GENERAL INFORMATION:

APPLICANT: C. Frank Bennett

APPLICANT: Elizabeth J. Ackermann

APPLICANT: Lex M. Cowser

TITLE OF INVENTION: ANTISENSE MODULATION OF CELLULAR INHIBITOR OF APOPTOSIS-2 EXPRESS

FILE REFERENCE: RTS-0021

CURRENT APPLICATION NUMBER: US/09/205,144

CURRENT FILING DATE: 1998-12-03

NUMBER OF SEQ ID NOS: 47

SEQ ID NO 1

LENGTH: 3076

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: CDS

LOCATION: (725)..(2539)

US-09-205-144-1

Query Match

Best Local Similarity 66.0%; Pred. No. 6.3e-19;

Matches 134; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 GAAGAAGCCAGATTGAAGTCAATTCAGAACTGGCCGGACTATGCTCATTTAACCCCCAGA 60

Db 1229 GAAATGCCAGATTACTTACTTTTCAGACATGGCC---ATTGACTTTTCTGTGCCCAACA 1285

QY 61 GAGTTAGCTAGTCTGCTGGCCTCTACTACAGAGGGGCTGATGATCAAGTCAATGCTTTTGT 120

Db 1286 GATCTGCAAAAGCAGGCTTTTACTACATAGGACCTGGAGACAGAGTGGCTTGGCTTGGC 1345

QY 121 TGTGGGGAAACTGAAATTTGGGAACCTGTGATCGTGGCTGGTGCAGAACACAGGAGA 180

Db 1346 TGTGTGGGAAATTTGAGCAATTTGGGAACCGAAGGATAATGCTATGTCAGAACACCTGAGA 1405
QY 181 CACTTTCCCAATTCGTTTTTGT 203
Db 1406 CATTITCCCAATGCCCATTTAT 1428

Search completed: April 16, 2003, 00:58:59

Job time : 30.6771 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:33:02 ; Search time 49.0521 Seconds
(without alignments)
3648.005 Million cell updates/sec

Title: US-09-654-743-50
Perfect score: 204
Sequence: 1 gaagaagccagattgaagtc.....ttcccaattgctttttgtt 204

Scoring table: IDENTITY_NUC
Gapex 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues

Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications, NA:*

- 1: /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	204	100.0	2100	9	US-09-201-936-9
2	204	100.0	2691	10	US-09-974-592-9
3	172	84.3	2540	9	US-09-201-936-3
4	172	84.3	5232	10	US-09-974-592-3
5	161	78.9	2404	9	US-09-964-899-38
6	81.4	39.9	2676	9	US-09-201-936-5
7	81.4	39.9	3076	9	US-09-954-531-16
8	81.4	39.9	3076	10	US-09-954-456-1635
9	81.4	39.9	6669	10	US-09-974-592-5
10	76.8	37.6	240	9	US-09-796-692-3493
11	75.2	36.9	240	9	US-09-796-692-3493
12	72.8	35.7	3151	10	US-09-974-592-13
13	71.8	35.2	2291	10	US-09-778-927A-21
14	71.8	35.2	2580	9	US-09-201-936-7
15	71.8	35.2	3532	10	US-09-880-107-3354
16	71.8	35.2	3732	10	US-09-974-592-7
17	71.2	34.9	2416	9	US-09-201-936-41
18	63	30.9	2450	9	US-09-201-936-39
19	63	30.9	2676	10	US-09-974-592-11

20	54.2	26.6	5504	8	US-08-913-322-1	Sequence 1, Appl
21	54.2	26.6	6124	8	US-08-913-322-21	Sequence 21, Appl
22	54.2	26.6	6124	10	US-09-967-768A-184	Sequence 184, Appl
23	54.2	26.6	6133	8	US-08-913-322-2	Sequence 2, Appl
24	54.2	26.6	6228	8	US-08-913-322-23	Sequence 23, Appl
25	51.2	25.1	3773	9	US-10-041-859-1	Sequence 1, Appl
26	35.6	17.5	176373	9	US-10-095-407-17	Sequence 17, Appl
27	34.8	17.1	152331	9	US-10-095-407-16	Sequence 16, Appl
28	33	16.2	616	10	US-09-867-701-1465	Sequence 1465, Ap
29	33	16.2	2880	10	US-09-925-301-415	Sequence 415, Ap
30	29.2	14.3	592	10	US-09-765-231A-9	Sequence 9, Appl
31	29.2	14.3	30310	10	US-09-800-631-96	Sequence 96, Appl
32	28.6	14.0	1086	10	US-09-815-242-6138	Sequence 6138, Ap
33	28.4	13.9	402	10	US-09-801-574-23	Sequence 23, Appl
34	28.2	13.8	1691139	9	US-10-067-514-1	Sequence 1, Appl
35	28	13.7	1559	10	US-09-867-550-1503	Sequence 1503, Ap
36	28	13.7	1656	9	US-10-038-072-239	Sequence 239, App
37	28	13.7	1656	9	US-10-121-049-239	Sequence 239, App
38	28	13.7	1656	9	US-10-123-904-239	Sequence 239, App
39	28	13.7	1656	9	US-10-140-470-239	Sequence 239, App
40	28	13.7	1656	9	US-10-175-746-239	Sequence 239, App
41	28	13.7	1656	9	US-10-176-918-239	Sequence 239, App
42	28	13.7	1656	9	US-10-176-921-239	Sequence 239, App
43	28	13.7	1656	9	US-10-137-865-239	Sequence 239, App
44	28	13.7	1656	9	US-10-140-474-239	Sequence 239, App
45	28	13.7	1656	9	US-10-142-431-239	Sequence 239, App

ALIGNMENTS

RESULT 1
US-09-201-936-9
; Sequence 9, Application US/09201936
; Publication No. US20020187946A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; FILE OF INVENTION: PROBES, AND DETECTION METHODS
; FILE REFERENCE: 07891/003003
; CURRENT APPLICATION NUMBER: US/09/201,936
; CURRENT FILING DATE: 1998-12-01
; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 9
; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9

Query Match	100.0%;	Score 204;	DB 9;	Length 2100;
Best Local Similarity	100.0%;	Pred. No. 1.3e-64;	Indels 0;	Gaps 0;
Matches 204;	Conservative 0;	Mismatches 0;		
QY	1	GAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCCGGACTATGCTCATTTAACCCCCAGA	60	
Db	613	GAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCCGGACTATGCTCATTTAACCCCCAGA	672	
QY	61	GAGTTAGCTAGTCTGGCCCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT	120	
Db	673	GAGTTAGCTAGTCTGGCCCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT	732	

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; EARLIER APPLICATION NUMBER: 09/011,356
; EARLIER FILING DATE: 1998-02-04
; EARLIER APPLICATION NUMBER: PCT/IB96/01022
; EARLIER FILING DATE: 1996-08-05
; EARLIER APPLICATION NUMBER: 08/576,956
; EARLIER FILING DATE: 1995-12-22
; EARLIER APPLICATION NUMBER: 08/511,485
; EARLIER FILING DATE: 1995-08-04
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: (2540)...(2540)
; OTHER INFORMATION: N may be any nucleotide
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US-09-201-936-3

Query Match      84.3%; Score 172; DB 9; Length 2540;
Best Local Similarity 90.2%; Pred.No. 7.6e-53;
Matches 184; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCAATTTAGAACTGGCCGGAGCTATGCTCATTTAACCCCCAGA 60
Db 520 GAAGAAGCTAGATTAAAGTCTCTTCAGAACTGGCCGACACTATGCTCACCTAACCCCAAGA 579
QY 61 GAGTTAGCTAGTGTGCGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120
Db 580 GAGTTAGCAAGTGTGCGACTCTACTACACAGGTATTGGTGACCAAGTGCAGTGTCTTTGT 639
QY 121 TGTGGGGGAAACAGTAAATTTGGGAACCTGTGATCGTGCCTGGTCAGACACAGGAGA 180
Db 640 TGTGGTGGAAACAGTAAATTTGGGAACCTGTGATCGTGCCTGGTCAGACACAGGCGA 699
QY 181 CACTTTCCCAATTGCTTTTGT 204
Db 700 CACTTTCCTAATTGCTTTTGT 723

RESULT 4
US-09-974-592-3
; Sequence 3, Application US/09974592
; Patent No. US2002012121
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAB5 AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 5232
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: variation
; LOCATION: 4623
; OTHER INFORMATION: n can be any nucleotide
; NAME/KEY: variation

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Query Match	84.3%	Score 172;	DB 10;	Length 5232;
Best Local Similarity	90.2%	Pred. No. 1e-52;		
Matches 184:	Conservative	0;	Mismatches 20;	Indels 0;
	Gaps			0;

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, CURRENT APPLICATION NUMBER: US/09/201,936.
, CURRENT FILING DATE: 1998-12-01
, EARLIER APPLICATION NUMBER: 09/011,356
, EARLIER FILING DATE: 1998-02-04
, EARLIER APPLICATION NUMBER: PCT/IB96/01022
, EARLIER FILING DATE: 1996-08-05
, EARLIER APPLICATION NUMBER: 08/576,956
, EARLIER FILING DATE: 1995-12-22
, EARLIER APPLICATION NUMBER: 08/511,485
, EARLIER FILING DATE: 1995-08-04
, NUMBER OF SEQ ID NOS: 45
, SOFTWARE: FastSeq for Windows Version 3.0
, SEQ ID NO 5
, LENGTH: 2676

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, NAME/KEY: variation
, LOCATION: (2470)...(2470)
, OTHER INFORMATION: N may be any nucleotide
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, FEATURE:
,
, NAME/KEY: variation
, LOCATION: (2476)...(2476)
, OTHER INFORMATION: N may be any nucleotide
,
, FEATURE:
,
, NAME/KEY: variation
, LOCATION: (2483)...(2483)
, OTHER INFORMATION: N may be any nucleotide
,
, FEATURE:
,
, NAME/KEY: variation
, LOCATION: (2602)...(2602)
, OTHER INFORMATION: N may be any nucleotide
,
, US-09-201-936-5

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Db	693	GA	AATGCCAGATTAC	TACTTTTTCAGAGCC	---ATTGACTTTTCTGTGCGCAACA	749
Qy	61	GAG	TAGTCTAGTGTG	CGCCCTCTACTACACAGGGGCTGATGATCAAGTGC	CAATGCTTTTGT	120
Db	750	GAT	CTGGCAGCAGCAG	CGCTTTTACTACATAGGACCTGGAGACAGAGTGC	CTTGTGCTTGGC	809
Qy	121	TGTGGGGGAAAC	TGAAAAATTGGGAAC	CGCTGTGTGTCCTGGTGCAGAACAGGAGA	180	
Db	810	TGTGTG	AAAAATTGACAATTGGGAAC	CGAATAATGCTATGTCAGAACACCTGAGA	869	
Qy	181	CAC	TTTCCCAANTGCTTTTTTGT	203		
bh	870	CAT	TTTCCCAANTGCTTTTTTGT	892		

; APPLICANT: Weaver, Zoe
 ; TITLE OF INVENTION: Process for Identifying
 ; TITLE OF INVENTION: Gene Sets
 ; FILE REFERENCE: 689290-77
 ; CURRENT APPLICATION NUMBER: US/09/954,531

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; SEQ ID NO 1635
; LENGTH: 3076
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-1635

Query Match          39.9%;   Score 81.4;   DB 10;   Length 3076;
Best Local Similarity 66.0%;   Pred. No. 1.5e-19;
Matches 134;   Conservative 0;   Mismatches 66;   Indels   3;   Gaps

QY  1  GAGAGCCAGATTGAAGTCATTTTCAGAACTGCGCGGACTATGCTCATTTTAACCCCCAGA  60
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Db   1229  GAAATGCCAGATTACTTACTTTTCAGACATGGCC---ATTGACCTTTTCTGTGCGCAACA  1285
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QY  61  GAGTGTAGCTAGTCTGGCCTCTACTACAGGGGCTGATGATCAAGTGCATGCTTTTGT  120
      |||  ||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   1286  GATCTGGCAAAACAGCGCTTTTACTACATAGAACCTGGAGACAGAGTGGCTTGTCTTCC  1345
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[illegible]

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? TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
? TITLE OF INVENTION: DISEASE
? FILE REFERENCE: 07891/009004
? CURRENT APPLICATION NUMBER: US/09/974,592
? CURRENT FILING DATE: 2001-10-09
? PRIOR APPLICATION NUMBER: US/09/617,053
? PRIOR FILING DATE: 2000-07-14
? PRIOR APPLICATION NUMBER: US/08/800,929
? PRIOR FILING DATE: 1997-02-13
? NUMBER OF SEQ ID NOS: 17
? SOFTWARE: FastSeq for Windows Version 4.0
? SEQ ID NO 5
? LENGTH: 6669
? TYPE: DNA
? ORGANISM: Homo sapiens
? FEATURE:
? NAME/KEY: variation
? LOCATION: (3677)...(3951)
? OTHER INFORMATION: n can be any nucleotide
US-09-974-592-5

Query Match          39.9%;   Score 81.4;   DB 10;   Length 6669;
Best Local Similarity 66.0%;   Pred. No. 2e-19;
Matches 134; Conservative    0; Mismatches 66; Indels      3; Gaps

QY      1 GAAGAGGCCAGATTGAAGTCATTTCACAGAACTGGCGGACTATGCTCATTTTAACCCCCAGA 60
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4725 GAAATGCCAGATTACTTACTTTTCAGACATGGCCC---ATTGACTTTTCTGTCCCAACA 4781

QY      61 GAGTTAGCTAGTCGTGGCCTCTACTACACAGGGGCTGATGATCAAGTGCAATGCTTTTGT 120
        ||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      4782 GATCTGGCACGACGAGGCTTTTACTACATAGGACCCTGGAGACAGAGTGGCTTGTCTTTGCC 4841

QY      121 TGTTGGGGAAAACCTGAAAAATTGGCAACCCCTGCTGCATCTCTGCTCTACAGACACAGAGA 180

```

Db 4842 TGTGGTGAATGACCAATGGACCAAGATAATCTATGTACAGACCTGAGA 4901

QY 181 CACTTCCCAATGCTTTTGT 203
Db 4902 CATTTCCTCAATGCCATTTAT 4924

RESULT 10
US-09-796-692-3493/c

; Sequence 3493, Application US/09796692

; Publication No. US20020198362A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY

; FILE REFERENCE: 2077.001200

; CURRENT APPLICATION NUMBER: US/09/796,692

; CURRENT FILING DATE: 2001-03-01

; PRIOR APPLICATION NUMBER: 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/222,903

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: 60/223,416

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: 60/223,378

; PRIOR FILING DATE: 2000-08-07

; NUMBER OF SEQ ID NOS: 9597

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 3493

; LENGTH: 240

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-796-692-3493

Query Match 37.6%; Score 76.8; DB 9; Length 240;

Best Local Similarity 67.5%; Pred. No. 2.4e-18;

Matches 108; Conservative 0; Mismatches 52; Indels 0; Gaps 0;

QY 44 CTCATTTAACCCCGAGAGATTAGTCTAGTGGCTCTACTACAGGGGCTGATGATC 103
Db 233 CTTTCTGTGCGCAACAGATCTGCAAAAGCAGGCTTTTACTACATAGGACCTGGAGACA 174

QY 104 AAGTGCATGCTTTTGTGGGGAACACTGAAATTTGGAACTTGGACCTGTGATCGTGCCT 163
Db 173 GAGTGGCTTGTCTTGTGGCTTGTGGCTTGTGGCTTGTGGCTTGTGGCTTGTGGCT 114

QY 164 GGTCAAGACACGAGACACTTCCCAATTTGCTTTTGT 203
Db 113 TGTCAAGACACCTGAGACATTTTCCCAATTTGCTTTTAT 74

RESULT 11

US-09-796-692-6687

; Sequence 6687, Application US/09796692

; Publication No. US20020198362A1

; GENERAL INFORMATION:

; APPLICANT: Gaiger, Alexander

; APPLICANT: Algate, Paul A.

; APPLICANT: Mannion, Jane

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND TH

; FILE REFERENCE: 2077.001200

; CURRENT APPLICATION NUMBER: US/09/796,692

; CURRENT FILING DATE: 2001-03-01

; PRIOR APPLICATION NUMBER: 60/186,126

; PRIOR FILING DATE: 2000-03-01

; PRIOR APPLICATION NUMBER: 60/190,479

; PRIOR FILING DATE: 2000-03-17

; PRIOR APPLICATION NUMBER: 60/200,545

; PRIOR FILING DATE: 2000-04-27

; PRIOR APPLICATION NUMBER: 60/200,303

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/200,779

; PRIOR FILING DATE: 2000-04-28

; PRIOR APPLICATION NUMBER: 60/200,999

; PRIOR FILING DATE: 2000-05-01

; PRIOR APPLICATION NUMBER: 60/202,084

; PRIOR FILING DATE: 2000-05-04

; PRIOR APPLICATION NUMBER: 60/206,201

; PRIOR FILING DATE: 2000-05-22

; PRIOR APPLICATION NUMBER: 60/218,950

; PRIOR FILING DATE: 2000-07-14

; PRIOR APPLICATION NUMBER: 60/222,903

; PRIOR FILING DATE: 2000-08-03

; PRIOR APPLICATION NUMBER: 60/223,416

; PRIOR FILING DATE: 2000-08-04

; PRIOR APPLICATION NUMBER: 60/223,378

; PRIOR FILING DATE: 2000-08-07

; NUMBER OF SEQ ID NOS: 9597

; SOFTWARE: FastSEQ for Windows Version 3.0

; SEQ ID NO 6687

; LENGTH: 240

; TYPE: DNA

; ORGANISM: Homo sapiens

; US-09-796-692-6687

Query Match 36.9%; Score 75.2; DB 9; Length 240;

Best Local Similarity 66.9%; Pred. No. 9.4e-18;

Matches 107; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 44 CTCATTTAACCCCGAGAGATTAGTCTAGTGGCTCTACTACAGGGGCTGATGATC 103
Db 8 CTTTCTGTGCGCAACAGATCTGCAAAAGCAGGCTTTTACTACATAGGACCTGGAGACA 67

QY 104 AAGTGCATGCTTTTGTGGGGAACACTGAAATTTGGAACTTGGACCTGTGATCGTGCCT 163
Db 68 GAGTGGCTTGTCTTGTGGCTTGTGGCTTGTGGCTTGTGGCTTGTGGCTTGTGGCT 127

QY 164 GGTCAAGACACGAGACACTTCCCAATTTGCTTTTGT 203
Db 128 TGTCAAGACACCTGAGACATTTTCCCAATTTGCTTTTAT 167

RESULT 12

US-09-974-592-13

; Sequence 13, Application US/09974592

; Patent No. US2002012012A1

; GENERAL INFORMATION:

; APPLICANT: Korneluk, Robert G

; APPLICANT: Mackenzie, Alexander E

; APPLICANT: Liston, Peter

; APPLICANT: Baird, Stephen

; APPLICANT: Tsang, Benjamin K

; APPLICANT: Pratt, Christine

; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS, AND

; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE

; TITLE OF INVENTION: DISEASE

```
FILE REFERENCE: 07891/009004
CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: US 09/617,053
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 3151
TYPE: DNA
ORGANISM: Mus musculus
US-09-974-592-13

Query Match 35.7%; Score 72.8; DB 10; Length 3151;
Best Local Similarity 61.7%; Pred. No. 2.1e-16;
Matches 116; Conservative 0; Mismatches 72; Indels 0; Gaps 0;

QY 7 GCCAGATTGAAGTCATTTCAGAACTGGCCGGACTATGCTCATTAAACCCCGAGAGATTGA 66
DB 1568 GCTCGATTGAGGACATTTCTGTACTGGCCACCTAGTGTCTCTTTCAGCCCGAGAGCTT 1627

QY 67 GCTAGTCTGGCCTCTACTACACAGGGGCTGATGATCAAGTGCATTCGCTTTTGTGGG 126
DB 1628 GCAAGTCTGGATCTATTACGTGGATCGCAATGATGATGATCAAGTGTCTTTTGTGAT 1687

QY 127 GGAAGAACTGAAATTTGGGAACCTCTGATCGTGGCTGTCAGAACACAGGACACTTT 186
DB 1688 GTGGCTTGAGATGTTGGGAACCTGGAGATGACCCCTGGATAGAACACGCCAAATGGTTT 1747

QY 187 CCCAATTG 194
DB 1748 CCAAGGTG 1755

RESULT 13
US-09-778-927A-21
Sequence 21, Application US/09778927A
Patent No. US20020068342A1
GENERAL INFORMATION:
APPLICANT: KHOSRAVI, Rafi et al.
TITLE OF INVENTION: NOVEL NUCLEIC ACID AND AMINO ACID SEQUENCES AND NOVEL
FILE REFERENCE: 2786-0160P
CURRENT APPLICATION NUMBER: US/09/778,927A
CURRENT FILING DATE: 2001-02-08
PRIOR FILING DATE: 2000-02-09
PRIOR APPLICATION NUMBER: IL134453
PRIOR FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 2291
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc.feature
LOCATION: (1)-(2291)
OTHER INFORMATION: n = a,c,g,t any unknown or other
US-09-778-927A-21

Query Match 35.2%; Score 71.8; DB 10; Length 2291;
Best Local Similarity 63.1%; Pred. No. 4.3e-16;
Matches 128; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 1 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCCGGACTATGCTCATTAAACCCCGAGA 60
DB 1922 GAAGAAGCCAGATTTCCTTACCACCATATGTGGCC---ATTAACTTTTGTCCACCATCA 1978

QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATTCGCTTTTGT 120
```

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DB 1979 GAATTGGCAGAGCTGGTTTTTATTATATAGACCTGGAGATAGGCTAGCTGCTTTGCC 2038
QY 121 TGTGGGGGAAACTGAAATTTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGAGA 180
DB 2039 TGTGCTGGGAAGCTCAGTAACCTGGGAACCGAAGGATAATGCTATGTCAGAACACCTGAGA 2098
QY 181 CACTTTCCCAATTCGTTTTTTGT 203
DB 2099 CATTTCCTCCCACTGTCCATTTTT 2121

RESULT 14
US-09-201-936-7
Sequence 7, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: MacKenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 7
LENGTH: 2580
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (2412)...(2412)
OTHER INFORMATION: N may be any nucleotide
US-09-201-936-7

Query Match 35.2%; Score 71.8; DB 9; Length 2580;
Best Local Similarity 63.1%; Pred. No. 4.6e-16;
Matches 128; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 1 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGGCCGGACTATGCTCATTAAACCCCGAGA 60
DB 787 GAAGAAGCCAGATTTCCTTACCACCATATGTGGCC---ATTAACTTTTGTCCACCATCA 843

QY 61 GAGTTAGCTAGTGGCTCTACTACACAGGGGCTGATGATCAAGTGCATTCGCTTTTGT 120
DB 844 GAATTGGCAAGAGCTGGTTTTTATTATATAGGACCTGGAGATAGGCTAGCTGCTTTGCC 903

QY 121 TGTGGGGGAAACTGAAATTTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGAGA 180
DB 904 TGTGTTGGGAAGCTCAGTAACCTGGGAACCAAGGATGATGCTATGTCAGAACACCGGAGG 963

QY 181 CACTTTCCCAATTCGTTTTTTGT 203
DB 964 CATTTCCTCCCACTGTCCATTTTT 986

RESULT 15
US-09-880-107-3354
Sequence 3354, Application US/09880107
Patent No. US20020142981A1
GENERAL INFORMATION:
APPLICANT: Horne, Darci T.
APPLICANT: Vockley, Joseph G.
```

Search completed: April 16, 2003, 01:03:57
Job time : 54.0521 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:12:47 ; Search time 976.083 Seconds

(Without alignments)
3384.833 Million cell updates/sec

Title: us-09-654-743-50
Perfect score: 204
Sequence: 1 gaagaagccagattgaagtc.....ttcccaattgtttttgtt 204

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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EST.*
1: em_estba.*
2: em_esthm.*
3: em_estin.*
4: em_estmu.*
5: em_estov.*
6: em_estpl.*
7: em_estro.*
8: em_esttc.*
9: gb_estl.*
10: gb_est2.*
11: gb_hic.*
12: gb_est3.*
13: gb_est4.*
14: gb_est5.*
15: em_estfun.*
16: em_estom.*
17: gb_gss.*
18: em_gss_hum.*
19: em_gss_inv.*
20: em_gss_pln.*
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25: em_gss_other.*
26: em_gss_pro.*
27: em_gss_fod.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	203	99.5	436	9	AI326613 mn83el2.y
2	193.4	94.8	375	9	AA097958
3	172	84.3	822	12	BG502660
4	150.2	73.6	1041	13	BM459898
5	144.2	70.7	1020	13	BM554544
6	118.2	57.9	1130	13	BM553272

7	97.2	47.6	742	13	BI329221
8	81.4	39.9	557	9	AI051610
9	81.4	39.9	886	14	BQ652590
10	79.2	38.8	593	13	BJ096099
11	78.2	38.3	567	13	BI961039
12	78.2	38.3	768	13	BM423292
13	77.2	37.8	459	13	BM446366
14	73.4	36.0	422	10	AW898626
15	72	35.3	298	12	BF016190
16	71.8	35.2	401	12	BF095673
17	71.8	35.2	889	14	BQ720079
18	71.8	35.2	895	14	BQ884287
19	71	34.8	959	13	BM458775
20	70.2	34.4	512	13	BI326908
21	70.2	34.4	611	13	BM536852
22	70.2	34.4	649	10	AW949508
23	69.8	34.2	837	12	BG743309
24	68.8	33.7	851	13	BI253303
25	68.8	33.7	896	14	BQ439248
26	68	33.3	286	9	AA473594
27	67	32.8	681	12	BF611032
28	66	32.4	673	9	AL640649
29	64.8	31.8	590	10	BE268377
30	64.8	31.8	953	17	CNS04211
31	64.4	31.6	936	14	C81977
32	64	31.4	450	12	BG729302
33	64	31.4	595	9	A1558531
34	62.4	30.6	592	13	BJ059822
35	62.2	29.5	441	13	BM312708
36	60.2	29.5	563	9	AA702174
37	60.2	29.5	652	10	AV704923
38	58.2	28.5	354	9	AA354707
39	57	27.9	302	14	R83677
40	57	27.9	780	13	BI771720
41	56.2	27.5	936	13	BM013796
42	55.4	27.2	341	10	AW375598
43	55.4	27.2	354	10	AW375594
44	55.4	27.2	402	10	AW846507
45	55.4	27.2	531	10	AW375599

ALIGNMENTS

RESULT 1
AI326613
LOCUS
DEFINITION
AI326613.1 GI:4061042
ACCESION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

AI326613
mn83el2.y1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
IMAGE:550702 5' similar to SW:IAPIX_MOUSE Q60989 X-LINKED INHIBITOR
OF APOPTOSIS PROTEIN ; mRNA sequence.

AI326613
EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Euthera; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 436)
Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
Geisels, S., Kucaba, T., Lacy, M., Le, M., Martin, J., Morris, M.,
Schellenberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
Thelising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
Waterston, R.

The WashU-HMHI Mouse EST Project
Unpublished (1996)
Contact: Marra M/Mouse EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LLNL ; contact the

IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:331494
 This read is a RESEQUENCE of a previously sequenced mouse clone
 This read has been verified (found to hit its original self in the
 correct orientation)
 Seq primer: -40RP from Gibco
 High quality sequence stop: 417.
 Location/Qualifiers
 1. .436

FEATURES

source

/organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:550702"
 /clone_lib="Stratagene mouse Tcell 937311"
 /tissue_type="Tcell"
 /dev_stage="M30 CD4+ cells"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: blood; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;
 Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGG
 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3' "

BASE COUNT 119 a 92 c 108 g 116 t 1 Others
 ORIGIN

Query Match 99.5%; Score 203; DB 9; Length 436;
 Best Local Similarity 99.5%; Pred. No. 2.8e-57;
 Matches 203; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGCGCGGACTATGCTCATTTAAACCCCGAGA 60
 Db 181 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGCGCGGACTATGCTCATTTAAACCCCGAGA 240
 QY 61 GAGTTAGCTAGTCTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 120
 Db 241 GAGTTAGCTAGTCTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 300
 QY 121 TGTGGGGGAAACTGAAAATTTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGGAGA 180
 Db 301 TGTGGGGGAAACTGAAAATTTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGGAGA 360
 QY 181 CACTTCCCAATTGCTTTTGT 204
 Db 361 CACTTCCCAATTGCTTTTGT 384

RESULT 2
 AA097958
 LOCUS
 DEFINITION
 mm89el2.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
 IMAGE:550702 5' similar to TR:G1145261 G1145261 MIHA. ;, mRNA
 sequence.
 AA097958
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 house mouse.
 Mus musculus

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 The WashU-HMI Mouse EST Project
 Unpublished (1996)
 Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@watson.wustl.edu

This clone is available royalty-free through LLNL ; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:331494
 Possible reversed clone: similarity on wrong strand
 Seq primer: -28ml3 rev1 Et from Amersham
 High quality sequence stop: 191.
 Location/Qualifiers
 1. .375

FEATURES

source

/organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:550702"
 /clone_lib="Stratagene mouse Tcell 937311"
 /tissue_type="Tcell"
 /dev_stage="M30 CD4+ cells"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: blood; Vector: pBluescript SK-; Site_1:
 EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
 Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;
 Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGG
 3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTT 3' "

BASE COUNT 109 a 86 c 89 g 91 t
 ORIGIN

Query Match 94.8%; Score 193.4; DB 9; Length 375;
 Best Local Similarity 99.5%; Pred. No. 4.4e-54;
 Matches 194; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGCGCGGACTATGCTCATTTAAACCCCGAGA 60
 Db 181 GAAGAAGCCAGATTGAAGTCATTTCAGAACTGCGCGGACTATGCTCATTTAAACCCCGAGA 240
 QY 61 GAGTTAGCTAGTCTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 120
 Db 241 GAGTTAGCTAGTCTGGCTCTACTACACAGGGGCTGATGATCAAGTCAATGCTTTTGT 300
 QY 121 TGTGGGGGAAACTGAAAATTTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGGAGA 180
 Db 301 TGTGGGGGAAACTGAAAATTTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGGAGA 360
 QY 181 CACTTCCCAATTGCTTTTGT 195
 Db 361 CACTTCCCAATTGCTTTTGT 375

RESULT 3
 BG502660
 LOCUS
 DEFINITION
 60234949DF1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4657102 5',
 mRNA sequence.
 BG502660
 ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 human.
 Homo sapiens

REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 COMMENT
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Robert Strausberg, Ph.D.
 Email: cgabbs@mail.nih.gov
 Tissue procurement: ATCC
 CDNA Library Preparation: CLONETECH Laboratories, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LLCMI449 row: c column: 23
 High quality sequence stop: 670.
 Location/Qualifiers
 1. .822

FEATURES
 source

OV	45	CATTTTAAACCC	CAGACAGT	TAGCTAG	TGCTGCTTACTACAC	GGCG-TGATGATCA	104
		Matches 133;	Conservative		Mismatches 23;	Indels 2;	Gaps 2;
		Best Local Similarity	84.28;	Pred. No.	1.4e-21;		

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Db 551 CACTTGAACCCGAGAGAGTGCCTGCCAGTGTGGCTGTACTACACAGGCACCTGATGACCA 610
QY 105 AGTGAATGCTTTTGTCTGGGGAAACTGAAATTTGGGAACCTGTGATCGTGCCCTG 164
Db 611 AGTCAGTGTCTGTCTGGGGAAACTGAAATTTGGGAACCTGTGATCGTGCCCTG 670
QY 165 GTCAGACACA-GGAGACACTTCCCAATTTGCTTTT 201
Db 671 GTCAGACACACGGAGACATTTCTCTAATTTGGTTCTT 708

RESULT 8
LOCUS AI051610/c 557 bp mRNA linear EST 10-JUL-1998
DEFINITION o202c09.x1 Soares fetal_liver_spleen_lNFLS.S1 Homo sapiens CDNA
clone IMAGE:1674160 3' similar to SW-1AFL1_HUMAN Q13489 INHIBITOR OF
APOPTOSIS PROTEIN 1 ;, mRNA sequence.
ACCESSION AI051610
VERSION AI051610.1 GI:3307144
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 557)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -40m3 fwd. Et from Amersham
High quality sequence stop: 436.

FEATURES
source
1..557
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1674160"
/clone_lib="Soares_fetal_liver_spleen_lNFLS.S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/notes="Organ: Liver and Spleen; vector: pT7T3D (Pharmacia)
with a modified polylinker; Site_1: Pac I; Site_2: Eco RI;
This is a subtracted version of the original Soares fetal
liver spleen lNFLS library. 1st strand cDNA was primed
with a Pac I - oligo(dT) primer [5',
AACTGGAGATTAATTAAGATCTTTTTTTTTTTTTTTT 3'],
double-stranded cDNA was ligated to Eco RI adaptors
(Pharmacia), digested with Pac I and cloned into the Pac I
and Eco RI sites of the modified pT7T3 vector. Library
went through one round of normalization. Library
constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 162 a 101 c 120 g 174 t
ORIGIN
Query Match 39.9%; Score 81.4; DB 9; Length 557;
Best Local Similarity 66.0%; Pred. No. 2.6e-16;
Matches 134; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 GAAGAGCCAGATTGAAGTCATTTTCAGAACTGGCCGGAGTATGCTCATTTAACCCCCAGA 60
Db 396 GAAATGCCAGATTACTTTTTCAGACATGGCC---ATTGACTTTTCTGTGCGCAACA 340
QY 61 GAGTTAGCTAGTCTGGCCCTCTACTACACAGGGCTGTATGATCAAGTCGAATGCTTTGT 120
Db 339 GATCTGGCAAAACGAGCGTTTACTACATAGGACCTGGAGAGATGGCTTCTGCTTGGC 280
QY 121 TGTGGGGAAACCTGAAAATTTGGGAACCTGTGTGCTGCTGGTGCAGAACACGAGAGA 180

```

```

Db 279 TGTGTGGAAAATTTGAGCAATTTGGGAACGGAAGGATAATGCTATGTCAGAACACCTGAGA 220
QY 181 CACTTTCCCAATTTGCTTTTGT 203
Db 219 CATTTTCCCAATTTGCCATTTAT 197

RESULT 9
LOCUS BO652590 886 bp mRNA linear EST 15-JUL-2002
DEFINITION AGENCOURT_8287942 NIH_MGC_100 Homo sapiens
5', mRNA sequence.
ACCESSION BO652590
VERSION BO652590.1 GI:21776762
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 886)
AUTHORS NIH-MGC http://mgs.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: CGAP (Stanford)
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLCM2508 row: g column: 18
High quality sequence stop: 638.

FEATURES
source
1..886
Location/Qualifiers
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:6298025"
/clone_lib="NIH_MGC_100"
/tissue_type="hepatocellular carcinoma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: liver; Vector: pONB7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally cloned
into ECORI/XhoI sites using the following 5' adaptor:
GGCAGAG(G). Size-selected >500bp for average insert size
1.8kb. Library constructed by Ling Hong in the laboratory
of Gerald M. Rubin (University of California, Berkeley)
using ZAP-cDNA synthesis kit (Stratagene) and Superscript
II RT (Life Technologies). Note: this is a NIH_MGC
Library."

BASE COUNT 255 a 193 c 186 g 250 t
ORIGIN
Query Match 39.9%; Score 81.4; DB 14; Length 886;
Best Local Similarity 66.0%; Pred. No. 3.2e-16;
Matches 134; Conservative 0; Mismatches 66; Indels 3; Gaps 1;

QY 1 GAAGAGCCAGATTGAAGTCATTTTCAGAACTGGCCGGAGTATGCTCATTTAACCCCCAGA 60
Db 239 GAAATGCCAGATTACTTTTTCAGACATGGCC---ATTGACTTTTCTGTGCGCAACA 295
QY 61 GAGTTAGCTAGTCTGGCCCTCTACTACACAGGGCTGTATGATCAAGTCGAATGCTTTGT 120
Db 296 GATCTGGCAAAACGAGCGTTTACTACATAGGACCTGGAGACAGAGTGGCTTCTGCTTGGC 355
QY 121 TGTGGGGAAACCTGAAAATTTGGGAACCTGTGTGCTGCTGGTGCAGAACACGAGAGA 180
Db 356 TGTGGTGGAAAATTTGAGCAATTTGGGAACCGAAGGATAATGCTATGTCAGAACACCTGAGA 415
QY 181 CACTTTCCCAATTTGCTTTTGT 203
Db 416 CATTTTCCCAATTTGCCATTTAT 438

```

```

RESULT 10
BJ096099
DEFINITION
  593 bp mRNA linear EST 12-DEC-2001
  Xenopus laevis cDNA clone XL152k19 5', mRNA sequence.
ACCESSION
  BJ096099
VERSION
  BJ096099.1 GI:17596868
KEYWORDS
  EST.
SOURCE
  African clawed frog.
ORGANISM
  Xenopus laevis
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
  Xenopodinae; Xenopus.
REFERENCE
  1 (bases 1 to 593)
  Kitayama, A., Terasaka, C., Mochii, M., Ueno, N., Shin-i, T. and Kohara
  Y.
  Expressed genes in X. laevis embryo
  Contact: Tadasu Shin-i
  Center For Genetic Resource Information
  National Institute of Genetics
  1111 Yata, Mishima, Shizuoka 411-8540, Japan
  Tel: 81-559-81-6856
  Fax: 81-559-81-6855
  Email: tshin@genes.nig.ac.jp.
FEATURES
  source
    Location/Qualifiers
    1..593
    /organism="Xenopus laevis"
    /db_xref="taxon:8355"
    /clone="XL152k19"
    /cclone_lib="NIBB Mochii normalized Xenopus early gastrula
    library"
    /tissue.type="whole embryo"
    /dev_stage="stage 10.5"
    /note="Vector: pBSRN3; Site_1: NotI; Site_2: EcoRI; cDNAs
    were oligo-dT primed and directionally cloned. Staging
    according to Nieuwkoop and Faber. Library is subtracted
    and was constructed by N. Garrett and A.M. Zorn,
    (Wellcome/CRC Institute)."
    BASE COUNT 175 a 129 c 137 g 152 t
    ORIGIN
      Query Match 38.8%; Score 79.2; DB 13; Length 593;
      Best Local Similarity 72.9%; Pred. No. 1.5e-15;
      Matches 102; Conservative 0; Mismatches 38; Indels 0; Gaps 0;
      QY 1 GAAGAGCCAGATTGAAGTCATTTCAGAACTGGCCGGCTGATGATCAAGTGCATGCTTTTGT 120
      || || || || || || || || || || || || || || || || || || || || || || ||
      Db 453 GAGGAAGCCAGACTGCAAAACATTTCAAAACCTGGCCAGGCTATTCGCCGTTAATGCCAAA 512
      QY 61 GAGTTAGCTAGTGGCTGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120
      || || || || || || || || || || || || || || || || || || || || || || ||
      Db 513 GAGCTTGCCAAATGACAGTCTCTTTTATACGATCAACGACCAAGTCAATGCTTTTGT 572
      QY 121 TGTGGGGAAACTGAAAAA 140
      || || || || || || || || || || || || || || || || || || || || || || ||
      Db 573 TGTGGTGAACAACTAATGAA 592

RESULT 11
BI961039
LOCUS
  MON01_5_C10.b1_A005 Monocytes (MON01) Equus caballus cDNA, mRNA
  sequence.
DEFINITION
  BI961039
ACCESSION
  BI961039
VERSION
  BI961039.1 GI:16319242
KEYWORDS
  EST.
SOURCE
  horse.
  Equus caballus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
REFERENCE
  1 (bases 1 to 567)
  Vandeplass, M.L., Cordonnier-Pratt, M.-M., Sudman, M.L., Wentzel, V.E.,
  Gingle, A.R., Pratt, L.H. and Moore, J.N.
  An EST database from equine (Equus caballus) monocytes
  Unpublished (2001)
  Contact: Cordonnier-Pratt MM
  Laboratory for Genomics and Bioinformatics
  The University of Georgia, Department of Plant Biology
  Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
  Tel: 706 542 1860
  Fax: 706 583 0210
  Email: mmpratt@uga.edu
  Sequences have been trimmed to exclude PolyA, vector and regions
  below phred quality 16. The threshold for high quality sequence is
  20. Three-prime sequences, which are obtained with PolyTmix or T7
  sequencing primer, are presented as the reverse complement.
  Seq primer: JEN REV
  High quality sequence stop: 534
  POLYA=No.
  Location/Qualifiers
  1..567
  /organism="Equus caballus"
  /db_xref="taxon:9796"
  /cclone_lib="Monocytes (MON01)"
  /cell_type="Isolated peripheral blood monocytes stimulated
  with E. coli lipopolysaccharide"
  /note="Vector: pBluescript SK(-) from Lambda ZapII;
  Site_1: XhoI; Site_2: EcoRI. The library was made from
  poly-A RNA in the cloning vector lambdaB ZapII. Clones to
  be sequenced were prepared by mass excision."
  BASE COUNT 147 a 130 c 136 g 154 t
  ORIGIN
    Query Match 38.3%; Score 78.2; DB 13; Length 567;
    Best Local Similarity 65.0%; Pred. No. 3.1e-15;
    Matches 132; Conservative 0; Mismatches 68; Indels 3; Gaps 1;
    QY 1 GAAGAGCCAGATTGAAGTCATTTCAGAACTGGCCGGCTGATGATCAAGTGCATGCTTTTGT 120
    || || || || || || || || || || || || || || || || || || || || || || ||
    Db 96 GAAAAGCCAGATTACTCATTTCAGATGTGGCG--CTGACCTTCTGTGCCCAACA 152
    QY 61 GAGTTAGCTAGTGGCTGCTCTACTACACAGGGGCTGATGATCAAGTGCATGCTTTTGT 120
    || || || || || || || || || || || || || || || || || || || || || || ||
    Db 153 GATCTGGCAAAAGCTGGCTTTTACTACATAGGACCGGGGACAGAGTGGCTGCTTTGCC 212
    QY 121 TGTGGGGAAACTGAAAAATTTGGGAACCTGTGATCGTCCCTGGTCAGAACACAGAGA 180
    || || || || || || || || || || || || || || || || || || || || || || ||
    Db 213 TGTGGTGGAAAATTGAGCAATTGGGAACCGGAGGATGATGCTATGTCGGAACACCTGAGA 272
    QY 181 CACTTTCCTCAATGCTTTTGT 203
    || || || || || || || || || || || || || || || || || || || || || || ||
    Db 273 CATTTCCTCAATGCTTTTGT 295

RESULT 12
BM423292
LOCUS
  PLATE4_F12 Rhesus Macaca mulatta cDNA, mRNA sequence.
DEFINITION
  BM423292
ACCESSION
  BM423292.1 GI:18392786
VERSION
  EST.
KEYWORDS
  EST.
SOURCE
  rhesus monkey.
  Macaca mulatta
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
  Cercopithecoinae; Macaca.
REFERENCE
  1 (bases 1 to 768)
  Katze, M.G., Bumgarner, R., Korth, M., Feldman, R., Amjadi, M. and
  Holzman, T.
  Expressed sequence tags from Rhesus macaque spleen
  Unpublished (2002)
  Contact: Holzman T
  Katze lab
  TITLE
  JOURNAL
  COMMENT
  
```

		Query Match	37.8%;	Score 77.2;	DB 13;	Length 459;
		Best Local Similarity	66.0%;	Pred. No. 6; 2e-15;		
		Matches 128;	Conservative	0;	Mismatches 63;	Indels
						3; Gaps 1;
QY	1	GAGAAGCCAGATTGAAGTCATTTTCAACAACGGCGGACTATGCTCATTTTAACCCCAGA	60			
Dd	269	GAAAAGCCAGATTACTTACCCTCAGATGTGGCGC	--TTGACTTTTCTGTCACCAACA	325		

QY 61 GAGTAGCTAGTGGCCTCTACTACACAGGGCTGATGATCAAGTGCAATGCTTTGT 120

DB	326	GACCTGGCCAAAGCAGGCTTTATTATCAATAGACCTTGGAGATAGATGGCTTGCCTTGGCC	383
QY	121	TGTGGGGGAAACCTGAAAAATTGGGAACCCCTGTGATGCTGGCTGGTCAGAACACAGGAGA	180

DG	360	TGTGGTGGACCATTTGGAGCCCGAGGAGTGATCTATG	CAGAACCCCTGAGA
QY	181	CACCTTCCCCAATTG	194

DD 440 CCCCCCCCCC 439

RESULT 14

LOCUS	AW898626	422 bp	linear	EST 24-MAY-2000
DEFINITION	RC1-NN0073-090500-012-e06	NN0073	Homo sapiens	cDNA, mRNA sequence.
ACCESSION	AW898626			

KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens

REFERENCE
AUTHORS
1 (bases 1 to 422)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordini, S., Costa, F.F.,
Nagai, M.A.,

Brunstein, A., deOliveira, P. S., Bucher, P., Jongeneel, C. V., O'Hare, M. J., Soares, F., Brentani, R. R., Reis, L. F., de Souza, S. J. and Simpson, A. J.

sequence tags
JOURNAL
PROC. NATL. ACAD. SCI. U.S.A. 97 (7), 3491-3496 (2000)
MEDLINE
20202663

Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,

Tel: +55-11-2704922
 Fax: +55-11-2707001
 Email: asimpson@ludwig.org.br
 www.ludwig.org.br

Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=st2-RC1-NN0073-090-
 500-012-e06&t3=2000-05-09&t4=1)
 500-012-e06&t3=2000-05-09&t4=1
 500-012-e06&t3=2000-05-09&t4=1

FEATURES
SOURCE
1
422
Location/Qualifiers
High quality sequence stop: 422.
High quality sequence start: 15
High quality sequence stop: 422.

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/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="NN0073"
/dev_stage="Adult"

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Site_2: SmaI; A mini-library was made by cloning products
/notes/Organ: nervous_normal; Vector: puc18; Site_1: SmaI;

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:40:42 ; Search time 698.026 Seconds
(without alignments)
5753.635 Million cell updates/sec

Title: US-09-654-743-48
Perfect score: 138
Sequence: 1 gagcagctaaagcgcctgca.....ttgacaagtgcccatgtgc 138

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2054640 seqs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*

1: gb.ba.*
2: gb.htg.*
3: gb.in.*
4: gb.om.*
5: gb.ov.*
6: gb.pat.*
7: gb.ph.*
8: gb.pl.*
9: gb.pr.*
10: gb.ro.*
11: gb.sts.*
12: gb.sy.*
13: gb.un.*
14: gb.vi.*
15: em.ba.*
16: em.fun.*
17: em.hum.*
18: em.in.*
19: em.mu.*
20: em.om.*
21: em.or.*
22: em.ov.*
23: em.pat.*
24: em.ph.*
25: em.pl.*
26: em.ro.*
27: em.sts.*
28: em.un.*
29: em.vi.*
30: em.htg_hum.*
31: em.htg_inv.*
32: em.htg_other.*
33: em.htg_mus.*
34: em.htg_pin.*
35: em.htg_rod.*
36: em.htg_mam.*
37: em.htg_vrt.*
38: em.sy.*
39: em.htgo_hum.*
40: em.htgo_mus.*
41: em.htgo_other.*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	138	100.0	1659	6	E31042	E31042 Method for
2	138	100.0	1659	9	BC032974	U32974 Human IAP-1
3	138	100.0	2086	9	BC032729	BC032729 Homo sapi
4	138	100.0	2404	6	AX429575	AX429575 Sequence
5	138	100.0	2540	6	AR103281	AR103281 Sequence
6	138	100.0	2540	6	AX412118	AX412118 Sequence
7	138	100.0	2540	9	HSU45880	AX45880 Human X-11a
8	138	100.0	3000	6	AX412131	AX412131 Sequence
9	138	100.0	5232	6	AR106397	AR106397 Sequence
10	138	100.0	5232	6	AR116899	AR116899 Sequence
11	138	100.0	122742	2	HS167819	Z93014 Homo sapien
12	138	100.0	133391	9	HSJ315G1	AL121601 Human DNA
13	138	100.0	201197	2	HS424J12	Z82207 Homo sapien
14	131.6	95.4	158093	9	AL390123	AL390123 Human DNA
15	130	94.2	1988	10	KMU36842	U36842 Mus musculu
16	128.4	93.0	1491	10	AF183429	AF183429 Rattus no
17	128.4	93.0	2032	10	AF304333	AF304333 Rattus no
18	128.4	93.0	2468	10	AB033366	AB033366 Rattus no
19	128.4	93.0	3032	10	AF304334	AF304334 Rattus no
20	128.4	93.0	185771	2	AC111718	AC111718 Rattus no
21	125.2	90.7	2100	6	AX412124	AX412124 Sequence
22	125.2	90.7	2691	6	AR106400	AR106400 Sequence
23	125.2	90.7	2691	6	AR116702	AR116702 Sequence
24	125.2	90.7	2691	10	KMU88990	U88990 Mus musculu
25	124.2	90.0	351	6	AX104966	AX104966 Sequence
26	122.6	88.8	351	6	AX104958	AX104958 Sequence
27	121	87.7	351	6	AX104964	AX104964 Sequence
28	119.4	86.5	1752	6	AX104956	AX104956 Sequence
29	119.4	86.5	1752	9	AF164681	AF164681 Homo sapi
30	119.4	86.5	154214	9	AC079753	AC079753 Homo sapi
31	117.8	85.4	351	6	AX104960	AX104960 Sequence
32	117.2	84.9	711	6	AR121220	AR121220 Sequence
33	117.2	84.9	711	6	AR123871	AR123871 Sequence
34	117.2	84.9	1758	6	AX370787	AX370787 Sequence
35	117.2	84.9	1758	6	AX370789	AX370789 Sequence
36	117.2	84.9	2032	9	AF420440	AF420440 Homo sapi
37	117.2	84.9	4993	9	AF104968	AF104968 Sequence
38	117.2	84.9	4993	9	AF164682	AF164682 Homo sapi
39	117.2	84.9	144301	9	AC010467	AC010467 Homo sapi
40	117.2	84.9	165662	9	AC092070	AC092070 Homo sapi
41	114	82.6	273	11	HUMSWX595	L24579 Human chrom
42	114	82.6	711	6	AX104970	AX104970 Sequence
43	114	82.6	711	6	AX104972	AX104972 Sequence
44	114	82.6	711	9	AY030052	AY030052 Pan trogl
45	114	82.6	711	9	AY030053	AY030053 Gorilla g

ALIGNMENTS

RESULT 1
E31042
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL

E31042
Method for screening substance inhibiting binding to XIAP.
E31042
E31042.1 GI:13017307
JP 1999326328-A/2.
unidentified.
unidentified.
unclassified.
1 (bases 1 to 1659)
Kunihiko M.
Method for screening substance inhibiting binding to XIAP
Patent: JP 1999326328-A 2 26-NOV-1999;
KUNIHICO MATSUMOTO

E31042
1659 bp
DNA
linear
PAT 18-JUN-2001

AKhter,N., Ayele,K., Beckstrom-Sternberg,S.M., Benjamin,B.,
Blakesley,R.W., Bouffard,G.G., Breen,K., Brinkley,C., Brooks,S.,
Dierich,N.L., Granite,S., Guan,X., Gupta,J., Haghighi,P.,
Hansen,N., Ho,S.-L., Karlins,E., Kwong,P., Laric,P., Legaspi,R.,
Maduro,Q.L., Mastello,C., Maskeri,B., Mastrian,S.D., McCloskey,J.C.,
McDowell,J., Pearson,R., Stantripop,S., Thomas,P.J., Touchman,J.W.,
Turgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Wiggins,L.,
Young,A., Zhang,L.-H. and Green,E.D.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAP Plate: 69 Row: j Column: 18
This clone was selected for full length sequencing because it
passed the following selection criteria: matched mRNA gi: 4502142.

FEATURES
source

Location/Qualifiers
1..2086
/organism="Homo sapiens"
/db_xref="LocusID:331"
/db_xref="taxon:9606"
/clone="MGC:45369 IMAGE:5532247"
/issue_type="uterus, leiomyosarcoma"
/clone_lib="NIH_MGC_71"
/lab_host="DH10B"
/note="Vector: pCMV-SPORT6"
79..1572
/codon_start=1
/product="baculoviral IAP repeat-containing 4"
/protein_id="AAH32729.1"
/db_xref="GI:21619764"
/translation="MTFNSFEKSKTCVPADINKEEFVEEFNRLKTFANPPSGSPVSA
STLARGFLYTGEGTVRCFSCSHAAVDHQYGDSDAVGRHKVSPNCRFNGFYLENSA
YSEEARLKGQYKVENYLGSDHFAIDRPSETHADYLLRTQGVVDISDTIIPNPFAM
EYRRHFPNCFVWLPYAHLPTELASGLYTGIGDQVQCFCGKGLKWEPCDDRAW
YVYNEQLARGFYALGEGDKVKFCGGLDWDKPSDEPWQSHAKYPCGKYLLEQK
GOEYINHLTHSLKLECLVTEKPSLFRIDDTIFONPMVOEAIRMGFSFKDKKI
MEEKTOISGNSVKSLEVLVADLVNAQKSDQESQTSIQKELSTEEQLRLQEEKLC
KICMDENIAIVFPGHLVTCQCAEAVDKPCMCYIVIFKQKIFNS"
BASE COUNT 689 a 341 c 450 g 606 t

CDS

Query Match 100.0%; Score 138; DB 9; Length 2086;
Best Local Similarity 100.0%; Pred. No. 2.4e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
LOCUS AX429575 2404 bp DNA linear PAT 21-JUN-2002
DEFINITION Sequence 38 from Patent WO0226820.
ACCESSION AX429575
VERSION AX429575.1 GI:21540833
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cohen,D., Dengler,U.J., Finelli,A.L., Freuler,F., Konsolaki,M.,
Reinhardt,M.W. and Zusan,S.
TITLE Transgenic drosophila melanogaster expressing beta amyloid

Query Match 100.0%; Score 138; DB 9; Length 2086;
Best Local Similarity 100.0%; Pred. No. 2.4e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
LOCUS AX429575 2404 bp DNA linear PAT 21-JUN-2002
DEFINITION Sequence 38 from Patent WO0226820.
ACCESSION AX429575
VERSION AX429575.1 GI:21540833
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cohen,D., Dengler,U.J., Finelli,A.L., Freuler,F., Konsolaki,M.,
Reinhardt,M.W. and Zusan,S.
TITLE Transgenic drosophila melanogaster expressing beta amyloid

Query Match 100.0%; Score 138; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.4e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
LOCUS AX412118 2540 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 218 from Patent WO0226968.
ACCESSION AX412118
VERSION AX412118.1 GI:21444581
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cohen,D., Dengler,U.J., Finelli,A.L., Freuler,F., Konsolaki,M.,
Reinhardt,M.W. and Zusan,S.
TITLE Transgenic drosophila melanogaster expressing beta amyloid

JOURNAL Patent: WO 0226820-A 38 04-APR-2002;
NOVARTIS ERFINO VERWALT GMBH (AT)
FEATURES
source
Location/Qualifiers
1..2404
/organism="Homo sapiens"
/db_xref="taxon:9606"
BASE COUNT 759 a 372 c 525 g 748 t
ORIGIN

Query Match 100.0%; Score 138; DB 6; Length 2404;
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Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
LOCUS AR103281 2540 bp DNA linear PAT 14-FEB-2001
DEFINITION Sequence 1 from patent US 6087173.
ACCESSION AR103281
VERSION AR103281.1 GI:12814869
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 2540)
AUTHORS Bennett,C.Frank, Ackermann,E.J. and Cowser,L.M.1
TITLE Antisense modulation of X-linked inhibitor of apoptosis expression
JOURNAL Patent: US 6087173-A 1 11-JUL-2000;
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BASE COUNT 781 a 415 c 571 g 773 t
ORIGIN

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Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
LOCUS AX412118 2540 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 218 from Patent WO0226968.
ACCESSION AX412118
VERSION AX412118.1 GI:21444581
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cohen,D., Dengler,U.J., Finelli,A.L., Freuler,F., Konsolaki,M.,
Reinhardt,M.W. and Zusan,S.
TITLE Transgenic drosophila melanogaster expressing beta amyloid

Query Match 100.0%; Score 138; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.4e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
LOCUS AX412118 2540 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 218 from Patent WO0226968.
ACCESSION AX412118
VERSION AX412118.1 GI:21444581
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cohen,D., Dengler,U.J., Finelli,A.L., Freuler,F., Konsolaki,M.,
Reinhardt,M.W. and Zusan,S.
TITLE Transgenic drosophila melanogaster expressing beta amyloid

Query Match 100.0%; Score 138; DB 6; Length 2540;
Best Local Similarity 100.0%; Pred. No. 2.4e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
LOCUS AX412118 2540 bp DNA linear PAT 14-JUN-2002
DEFINITION Sequence 218 from Patent WO0226968.
ACCESSION AX412118
VERSION AX412118.1 GI:21444581
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Cohen,D., Dengler,U.J., Finelli,A.L., Freuler,F., Konsolaki,M.,
Reinhardt,M.W. and Zusan,S.
TITLE Transgenic drosophila melanogaster expressing beta amyloid


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/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="X"
/map="q25"
/clone="RPI-167P19"
/clone_lib="RPCI-1"
1. .18344
/note="assembly_fragment:00897
fragment_chain:1"
1845..24822
/note="assembly_fragment:03100
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24923..26984
/note="assembly_fragment:01003
fragment_chain:2"
27085..36741
/note="assembly_fragment:01036
fragment_chain:2"
36842..40798
/note="assembly_fragment:02480
fragment_chain:3"
40899..50764
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61009..90700
/note="assembly_fragment:00910"
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/note="assembly_fragment:02641"

BASE COUNT 34749 a 24137 c 25101 g 37853 t 902 others
ORIGIN

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Best Local Similarity 100.0%; Pred. No. 2e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
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Db 88514 GAGCAGCTAAGGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 88455
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QY 61 GCATCTCTTTTGTCTCTGTCGACATCTAGTCTGTTGTAACAATGCTGTAAGCAGATT 120
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Db 88454 GCATCTCTTTTGTCTCTGTCGACATCTAGTCTGTTGTAACAATGCTGTAAGCAGATT 88395
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QY 121 GACAAGTGTCCCATGTGC 138
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Db 88394 GACAAGTGTCCCATGTGC 88377

RESULT 12
HSDJ315G1 133391 bp DNA linear PRI 23-JUN-2000
LOCUS Human DNA sequence from clone RPI-315G1 on chromosome Xq24-25.
DEFINITION Contains a PDZ (DHR, GLGF) domain protein pseudogene, the API3 gene
for apoptosis inhibitor 3 (XIAP, HILP), a putative novel gene,
ESTs, STSS, GSSs and a putative cpG island, complete sequence.
ACCESSION AL121601
VERSION AL121601.13 GI:7159760
KEYWORDS HTG; API3; CpG island; DHR; GLGF; HILP; PDZ; XIAP.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 133391)
AUTHORS Grafham D.
TITLE Direct Submission
JOURNAL Submitted (12-APR-2000) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk

COMMENT
On Mar 6, 2000 this sequence version replaced gi:6983378.
During sequence assembly data is compared from overlapping clones.
Where differences are found these are annotated as variations
together with a note of the overlapping clone name. Note that the
variation annotation may not be found in the sequence submission
corresponding to the overlapping clone, as we submit sequences with
only a small overlap as described above.
This sequence has been finished according to sequence map criteria
as follows. An attempt is made to resolve all sequencing problems,
such as compressions and repeats, but not necessarily within known
annotated human repeat sequence elements (e.g. Alu). Where the
sequence is ambiguous, there is an annotation using the 'unsure'
feature key.
The following abbreviations are used to associate primary accession
numbers given in the feature table with their source databases:
Em: EMBL; Sv: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information
on the WORMPEP database can be found at
http://www.sanger.ac.uk/projects/Celegans/wormpep This sequence
was generated from part of bacterial clone contigs of human
chromosome X, constructed by the Sanger Centre Chromosome X Mapping
Group. Further information can be found at
http://www.sanger.ac.uk/HGP/ChrX
RPI-315G1 is from the library RPCI-1 constructed at the Roswell
Park Cancer Institute by the group of Pieter de Jong. For further
details see http://bacpac.med.buffalo.edu/
VECTOR: pCYPAC2
This sequence is the entire insert of clone RPI-315G1 The true
right end of clone RP6-30A23 is at 100 in this sequence.

FEATURES
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1. .133391
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/clone_lib="RPCI-1"
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misc_feature 4624..4824
/note="match: GSS: Em:AQ587673"
misc_feature 4828..5111
/note="match: GSS: Em:AQ587673"
gene complement(6712..7417)
/gene="dJ315G1.1"
CDS complement(6712..7417)
/gene="dJ315G1.1"
/note="dJ315G1.1 (PDZ (DHR, GLGF) domain protein
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match: ESTs: Em:AW369746
match: proteins: Tr:Q9Y510 Tr:O14911 Tr:Q9Z101 Tr:O18129
Tr:O97111"
/pseudo
/codon_start=1
/evidence=not_experimental
gene 13544..36179
/gene="API3"
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28615..28815,35110..36179)
/gene="API3"
/product="dJ315G1.2 (apoptosis inhibitor 3 (XIAP, HILP))"
/note="match: cDNAs: Em:AB033366 Em:U88990 Em:U32974
Em:U45880 Em:U36842
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Em:A1598959 Em:A1418337 Em:A1277821 Em:HSCZQG052
Em:AA987840"
/evidence=not_experimental
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28615..28815,35110..35303)
/gene="API3"
CDS

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Sw:Q13490 Sw:Q60989 Sw:Q62210"
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/db_xref="GI:8744934"
/translation="MTNSPEGSKTCVPADINKEEFVEEPRNLKTRANFPSPGSPVSA
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YSEARLKSFQNDYAHITPRELASAGLYTIGDQVQCFCGKLNKWPEDRAWNS
EHRHFPNCFVLGNLIRSEDAVSDFNPNSTNLPNPSMADYEARTFTGTWI
YSVNKEOLARAGVLEGDKVCFHCGGLTDMKPSDPEQHAQWPGCKYLLLEOK
QYEVINIHLSLECLVTRTEKPSLTRLIDDTIFQNPVQEAIRMGFSGFKDKKI
MEEKIQISKLVLEVLVADLVNAQKSMODESSQTSLOKEISTEQLRLRLEKLC
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28618..28815))
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/note="90 copies 2 mer ta 73% conserved"
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/misc_feature
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29663..29811
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31721..31780
/note="match: STS: Em:L24583"
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38208..38451
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complement(40058..40218)
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Best Local Similarity 100.0%; Pred No. 2e-30;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTTGGCAAATCTGTATGATAGAAATATT 60
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QY 61 GCTATCGTTTTTGTCTTCTTGACATCTAGTCACTGTAAACAATGCTGCTGAAGCAGTT 120
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Db 35184 GCTATCGTTTTTGTCTTCTTGACATCTAGTCACTGTAAACAATGCTGCTGAAGCAGTT 35243
QY 121 GACAAGTGTCCTCATGTGC 138
|||||
Db 35244 GACAAGTGTCCTCATGTGC 35261
RESULT 13
HS424J12/c
LOCUS
DEFINITION
Homo sapiens chromosome X clone RP3-424J12, *** SEQUENCING IN
PROGRESS ***, 15 unordered pieces.
ACCESSION
282207
VERSION
282207.3 GI:12331276
KEYWORDS
HTG; HTGS_PHASE1; HTGS_CANCELLED.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 201197)
AUTHORS
Grafham D.
TITLE
Direct Submission
JOURNAL
Submitted (09-JUL-2001) Sanger Centre, Hinxton, Cambridgeshire,
CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
requests: clonerequest@sanger.ac.uk
COMMENT
On Jan 22, 2001 this sequence version replaced gi:10045116.
```

----- Genome Center
 Center: Sanger Centre
 Center code: SC
 Web site: <http://www.sanger.ac.uk>
 Contact: humqueres@sanger.ac.uk
 ----- Project Information
 Center project name: DJ424J12
 ----- Summary Statistics

Assembly program: XGAP4; version 4.5
 Sequencing vector: MJ3; M7815; 74% of reads
 Sequencing vector: plasmid; L08752; 25% of reads
 Chemistry: Dye-terminator Big Dye; 0% of reads
 Chemistry: Dye-terminator ABI; 96% of reads
 Chemistry: Dye-terminator ABI; 96% of reads
 Chemistry: Dye-terminator ABI; 96% of reads
 Consensus quality: 194333 bases at least Q40
 Consensus quality: 196512 bases at least Q30
 Consensus quality: 198047 bases at least Q20
 Insert size: 199797; sum-of-contigs
 Quality coverage: 6.87x in Q20 bases; sum-of-contigs

* NOTE: This is a 'working draft' sequence. It currently
 * consists of 15 contigs. The true order of the pieces
 * is not known and their order in this sequence record is
 * arbitrary. Gaps between the contigs are represented as
 * runs of N, but the exact sizes of the gaps are unknown.
 * This record will be updated with the finished sequence
 * as soon as it is available and the accession number will
 * be preserved.

1 4154: contig of 4154 bp in length
 * 4155 4254: gap of 100 bp
 * 4255 18703: contig of 14449 bp in length
 * 18704 18803: gap of 100 bp
 * 18804 20941: contig of 2138 bp in length
 * 20942 21041: gap of 100 bp
 * 21042 34907: contig of 13866 bp in length
 * 34908 35012: gap of 105 bp
 * 35013 37508: contig of 2496 bp in length
 * 37509 37608: gap of 100 bp
 * 37609 52739: contig of 15131 bp in length
 * 52740 52839: gap of 100 bp
 * 52840 56933: contig of 4094 bp in length
 * 56934 57033: gap of 100 bp
 * 57034 88245: contig of 31212 bp in length
 * 88246 88346: gap of 101 bp
 * 88347 93386: contig of 5040 bp in length
 * 93387 93486: gap of 100 bp
 * 93487 123956: contig of 30470 bp in length
 * 123957 124056: gap of 100 bp
 * 124057 147917: contig of 23861 bp in length
 * 147918 148017: gap of 100 bp
 * 148018 176236: contig of 28219 bp in length
 * 176237 176336: gap of 100 bp
 * 176337 187128: contig of 10792 bp in length
 * 187129 187228: gap of 100 bp
 * 187229 190824: contig of 3596 bp in length
 * 190825 190959: gap of 135 bp
 * 190960 201197: contig of 10238 bp in length.

FEATURES

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 /clone_lib="RPCI-3"
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 4255. .18703
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 fragment_chain:1"
 18804. .20941
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 fragment_chain:2"
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 37609. .52739
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 57034. .88245
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 148018. .176236
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 vector_side:right"
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 Best Local Similarity 100.0%; Pred. No. 1.9e-30;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 Db 154102 GCTATCGTTTTTCTCTCTGTCGACATCTAGTCACATGTGTAACAATCTGCTGAAGCAGTT 154043
 QY 121 GACAAGTGTCCCATGTGC 138
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 Db 154042 GACAAGTGTCCCATGTGC 154025
 RESULT 14
 AL390123
 LOCUS
 DEFINITION Human DNA sequence from clone RP11-566F5 on chromosome 10, complete
 sequence.
 ACCESSION AL390123
 VERSION AL390123.14 GI:16304934
 KEYWORDS HTG.
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 158093)
 Laid, G.
 Direct Submission
 Submitted (19-OCT-2001) Sanger Centre, Hinxton, Cambridgeshire,
 CB10 1SA, UK. E-mail enquiries: humqueres@sanger.ac.uk
 requests: clonerequests@sanger.ac.uk
 On Oct 21, 2001 this sequence version replaced gi:15020926.
 During sequence assembly data is compared from overlapping clones.
 Where differences are found these are annotated as variations
 together with a note of the overlapping clone name. Note that the
 variation annotation may not be found in the sequence submission
 corresponding to the overlapping clone, as we submit sequences with
 only a small overlap as described above.

This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em: EMBL; Sw: SWISSPROT; Tr: TrEMBL; Wp: WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep. This sequence was generated from part of bacterial clone contigs of human chromosome 10, constructed by the Sanger Centre Chromosome 10 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr10>. RP11-566F5 is from the library RP11-11.2 constructed by the group of Pieter de Jong. For further details see <http://www.chori.org/bacpac/home.htm>. VECTOR: pBACE3.6

IMPORTANT: This sequence is not the entire insert of clone RP11-566F5. It may be shorter because we sequence overlapping sections only once, except for a short overlap. The true left end of clone RP11-271113 is at 156094 in this sequence. The true right end of clone RP11-402N18 is at 2000 in this sequence.

FEATURES Location/Qualifiers
 source 1. .158093

 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="10"
 /clone="RP11-566F5"
 /clone_lib="RP11-11.2"
 BASE COUNT 49096 a 31903 c 31075 g 46019 t
 ORIGIN

Query Match 95.4%; Score 131.6; DB 9; Length 158093;
 Best Local Similarity 97.1%; Pred. No. 1.5e-28;
 Matches 134; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
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 Db 89067 GAGCAGCTAGGACCTGCAAGTGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 89126
 |||||||

QY 61 GCTATCGTTTTTGTCTCTGTCGACATCTAGTCACTTGTAAACAATGTCTGAAGCAGTT 120
 |||||||

Db 89127 GCTATCGTTTTTGTCTCTGTCGACATCTAGTCACTTGTAAACAATGTCTGAAGCAGTT 89186
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QY 121 GACAAGTGTCCTCATGTGC 138
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Db 89187 GACAAGTGTCCTCATGTGC 89204
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RESULT 15
 LOCUS MMU36842 1988 bp mRNA linear ROD 05-JUN-1996
 DEFINITION Mus musculus IAP homolog A (MIHA) mRNA, complete cds.
 ACCESSION U36842
 VERSION U36842.1 GI:1145260
 KEYWORDS house mouse strain-C57 Black 6 x CBA.
 SOURCE Mus musculus
 ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 REFERENCE 1 (bases 1 to 1988)
 AUTHORS Uren,A.G., Pakusch,M., Hawkins,C.J., Puls,K.L. and Vaux,D.L.
 TITLE Cloning and expression of apoptosis inhibitory protein homologs
 that function to inhibit apoptosis and/or bind tumor necrosis
 factor receptor-associated factors
 JOURNAL Proc. Natl. Acad. Sci. U.S.A. 93 (10), 4974-4978 (1996)
 MEDLINE 96209843
 PUBMED 8643514
 REFERENCE 2 (bases 1 to 1988)

AUTHORS Vaux,D.L., Uren,A.G. and Pakusch,M.
 TITLE Direct Submission
 JOURNAL Submitted (21-SEP-1995) M. Pakusch, The Walter and Eliza Hall
 Institute, Royal Parade, Parkville, Victoria 3050, Australia
 FEATURES Location/Qualifiers
 source 1. .1988

 /organism="Mus musculus"
 /strain="C57 Black 6 x CBA"
 /db_xref="taxon:10090"
 /sex="female"
 /tissue_type="liver"
 /dev_stage="6-8 weeks old"
 gene 1. .1988
 /genes="MIHA"
 CDS 212..1702
 /genes="MIHA"
 /notes="apoptosis inhibitor; homolog of Baculovirus IAP
 protein"

 /codon_start=1
 /product="MIHA"
 /protein_id="AAC52594.1"
 /db_xref="GI:1145261"
 /translation="MTFNSFEGTRIFVLADTKNDEEFVEFNRLKTFANFPSSPVSA
 STLRAGFLYTGEGTVQCFSCAAIDRWYGDGSAVHRHRISPNCRFINGFFENGA
 CSGEARLKSFQNPDPYAHLTRELASAGLYTGDQVQFCGCGKLEWPCDRAMS
 EHRHFPNCFVLRNVNVRSEGVSSDRNFNSTNSPNPAAAEYKATVITFGTWT
 SYNKEQLARAGYALGEGKVKCFHCGGGLTDWKPSEDPEQHAKEVYPCCKVILLDEK
 QEIYNNIHLTHSLEESLGAETKTPSLTKKIDITIFQNPVQEAIRMGFSFKDKITM
 EKIQTSGSYLSLEVLIALDLSAQDNTEDESSQSLQKIDISTEQRLRLQEKELCK
 ICMDRNAIVFVPCGHLVTCQCAEAVDKPCMCYTVITFKQKIFMS"

misc_feature 287..490
 /genes="MIHA"
 /notes="BIR repeat 1"
 698..901
 misc_feature /genes="MIHA"
 /notes="BIR repeat 2"
 1001..1198
 misc_feature /genes="MIHA"
 /notes="BIR repeat 3"
 1556..1660
 misc_feature /genes="MIHA"
 /notes="RING finger"

BASE COUNT 505 a 367 c 459 g 557 t
 ORIGIN

Query Match 94.2%; Score 130; DB 10; Length 1988;
 Best Local Similarity 96.4%; Pred. No. 5.6e-28;
 Matches 133; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
 |||||||

Db 1523 GAGCAGCTAAGGCGCTTACAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 1582
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QY 61 GCTATCGTTTTTGTCTCTGTCGACATCTAGTCACTTGTAAACAATGTCTGAAGCAGTT 120
 |||||||

Db 1583 GCTATCGTTTTTGTCTCTGTCGACATCTAGTCACTTGTAAACAATGTCTGAAGCAGTT 1642
 |||||||

QY 121 GACAAGTGTCCTCATGTGC 138
 |||||||

Db 1643 GACAAGTGTCCTCATGTGC 1660
 |||||||

Search completed: April 15, 2003, 23:25:21
 Job time : 765.026 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 19:38:17 ; Search time 92.2396 Seconds
(without alignments)
3369.223 Million cell updates/sec

Title: US-09-654-743-48
Perfect score: 138
Sequence: 1 gagcagctaaagcgccgtgca.....ttgacaagtgtcccatgtgc 138

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

Total number of hits satisfying chosen parameters: 4370478

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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24: /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
C 1	138	100.0	489	22	ABA43584 Human breast cell
C 2	138	100.0	489	22	AAI12335 Probe #2268 for ge
C 3	138	100.0	489	22	AAI02249 Probe #2240 used t
4	138	100.0	1533	23	AA574582 DNA encoding novel
5	138	100.0	1533	23	AA588274 DNA encoding novel
6	138	100.0	1659	21	AAZ48862 Human XIAP coding
7	138	100.0	2404	24	AAK99405 DNA of APP related
8	138	100.0	2540	18	AAK70836 Human apoptosis in
9	138	100.0	2540	21	AAA64901 Human X-linked inh

10	138	100.0	2540	24	ABK93869 Human cDNA encodin
11	138	100.0	3000	24	ABK93875 Human cDNA encodin
12	138	100.0	5232	19	AAV55038 Human XIAP coding
C 13	134	97.1	148	22	ABA48694 Human breast cell
C 14	134	97.1	148	22	AAI21530 Probe #11463 for g
C 15	134	97.1	148	22	AAI07226 Probe #7217 used t
16	130	94.2	1988	18	AAI72710 Mouse inhibitor of
17	125.2	90.7	2100	18	AAK70839 Mouse apoptosis in
18	125.2	90.7	2100	24	ABK93872 Mouse cDNA encodin
19	125.2	90.7	2691	19	AAV55041 Murine XIAP coding
20	124.2	90.0	351	22	AAK03580 Rhesus IAP-like pr
21	122.6	88.8	351	22	AAK03576 Baboon IAP-like pr
22	121	87.7	351	22	AAK03579 Gorilla IAP-like p
23	119.4	86.5	802	20	AAK03018 Human IL-1ra BAC c
24	119.4	86.5	1752	22	AAK03575 Human IAP-like pro
C 25	119.4	86.5	2211	20	AAK02975 Human IL-1ra BAC c
26	117.8	85.4	351	22	AAK03577 Chimpanzee IAP-lik
27	117.2	84.9	711	21	AAA06940 DNA encoding human
28	117.2	84.9	1559	24	ABK13197 Human testes speci
29	117.2	84.9	1758	24	ABK14677 Human inhibitor of
30	117.2	84.9	1758	24	ABK14678 Human inhibitor of
31	117.2	84.9	4993	22	AAK03581 Human IAP-like pro
32	114	82.6	711	22	AAK03582 Chimpanzee IAP-lik
33	114	82.6	711	22	AAK03583 Gorilla IAP-like p
34	108.2	78.4	348	22	AAK03578 Cynomolgus IAP-lik
35	61.2	44.3	2416	18	AAI70841 Mouse apoptosis in
36	61.2	44.3	2416	24	ABK93874 Mouse cDNA encodin
37	61.2	44.3	2862	18	AAI61592 Murine c-IAP. Mus
38	61.2	44.3	3151	19	AAV55043 Murine XIAP-2 codi
39	60.2	43.6	2474	18	AAK70840 Mouse apoptosis in
40	60.2	43.6	2474	24	ABK93873 Mouse cDNA encodin
41	58.6	42.5	2601	18	AAI61591 Human c-IAP2. Hom
42	58.6	42.5	2676	19	AAV55042 Murine XIAP-1 codi
43	58.6	42.5	3076	18	AAI72712 Human inhibitor of
44	58.6	42.5	3076	20	AAZ41005 Human cellular inh
45	58.6	42.5	3076	20	AAZ22096 Human cellular inh

ALIGNMENTS

RESULT 1
ABA43584/C
ID ABA43584 standard; DNA; 489 BP.
XX AC ABA43584;
XX AC
DT 01-FEB-2002 (first entry)
XX XX
DE Human breast cell single exon nucleic acid probe #2279.
XX XX
KW Human; microarray; single exon probe; gene expression; breast;
XX disease; cancer; ss.
XX Homo sapiens.
XX XX
PN WC200157271-A2.
XX XX
PD 09-AUG-2001.
XX XX
PF 30-JAN-2001; 2001WO-US00662.
XX XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234587.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI

(MOLE-) MOLECULAR DYNAMICS INC.

Penn SG, Hanzel DK, Chen W, Rank DR;
WPI; 2001-476286/51.
Novel single exon nucleic acid probe used to measuring gene expression
in a human breast -
Claim 25; SEQ ID No 2240; 322pp; English.
The present invention relates to novel single exon nucleic acid probes.
The present sequence is one such probe. The probes are useful for
measuring human gene expression in a human breast sample, where the probe
hybridizes at high stringency to a nucleic acid expressed in the human
breast. The probes are useful for predicting, diagnosing, grading,
staging, monitoring and prognosing diseases of the human breast,
particularly those diseases with polygenic aetiology. The diseases
include: breast cancer, disorders of development, inflammatory diseases
of the breast, fibrocystic changes, proliferative breast disease and
non-carcinoma tumours.
CC Note: The sequence data for this patent did not form part of the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
Sequence 489 BP; 175 A; 90 C; 73 G; 151 T; 0 other;
Query Match 100.0%; Score 138; DB 22; Length 489;
Best Local Similarity 100.0%; Pred. No. 9.4e-34;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGAGCTTTGC AAAATCTGTATGGATAGAATAATT 60
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DB 450 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGCTTTGC AAAATCTGTATGGATAGAATAATT 391
|||||
QY 61 GCTATCGTTTTTTCCTTGTCGACATCTAGTCACCTTTGTAACAATGTGCTGAAGCAGTT 120
|||||
DB 390 GCTATCGTTTTTTCCTTGTCGACATCTAGTCACCTTTGTAACAATGTGCTGAAGCAGTT 331
|||||
QY 121 GACAAGTGCCCCATGTGC 138
|||||
DB 330 GACAAGTGCCCCATGTGC 313
|||||

RESULT 4
AAS74582
ID AAS74582 standard; cDNA; 1533 BP.
XX AC AAS74582;
XX DT 13-FEB-2002 (first entry)
DE DNA encoding novel human diagnostic protein #10386.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
OS
XX WO200175067-A2.
PN 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
PA Drmanac RT, Liu C, Tang YT;
PI WPTI; 2001-639362/73.
XX

P-PSDB; ABGI0395.
New isolated polynucleotide and encoded polypeptides, useful in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits and to assess
biodiversity -
Claim 1; SEQ ID No 10386; 103pp; English.
The invention relates to isolated polynucleotide (I) and
polypeptide (II) sequences. (I) is useful as hybridisation probes,
polymerase chain reaction (PCR) primers, oligomers, and for chromosome
and gene mapping, and in recombinant production of (II). The
polynucleotides are also used in diagnostics as expressed sequence tags
for identifying expressed genes. (I) is useful in gene therapy techniques
to restore normal activity of (II) or to treat disease states involving
(II). (II) is useful for generating antibodies against it, detecting or
quantitating a polypeptide in tissue, as molecular weight markers and as
a food supplement. (II) and its binding partners are useful in medical
imaging of sites expressing (II). (I) and (II) are useful for treating
disorders involving aberrant protein expression or biological activity.
The polypeptide and polynucleotide sequences have applications in
diagnostics, forensics, gene mapping, identification of mutations
responsible for genetic disorders or other traits to assess biodiversity
and to produce other types of data and products dependent on DNA and
amino acid sequences. AAS64197-AAS94364 represent novel human
diagnostic coding sequences of the invention.
Note: The sequence data for this patent did not appear in the printed
specification, but was obtained in electronic format directly from WIPO
at ftp.wipo.int/pub/published_pct_sequences.
Sequence 1533 BP; 362 A; 421 C; 392 G; 358 T; 0 other;
Query Match 100.0%; Score 138; DB 23; Length 1533;
Best Local Similarity 100.0%; Pred. No. 1.3e-33;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGAGCTTTGC AAAATCTGTATGGATAGAATAATT 60
|||||
DB 1354 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGAGCTTTGC AAAATCTGTATGGATAGAATAATT 1413
|||||
QY 61 GCTATCGTTTTTTCCTTGTCGACATCTAGTCACCTTTGTAACAATGTGCTGAAGCAGTT 120
|||||
DB 1414 GCTATCGTTTTTTCCTTGTCGACATCTAGTCACCTTTGTAACAATGTGCTGAAGCAGTT 1473
|||||
QY 121 GACAAGTGCCCCATGTGC 138
|||||
DB 1474 GACAAGTGCCCCATGTGC 1491
|||||

RESULT 5
AAS88274
ID AAS88274 standard; cDNA; 1533 BP.
XX AC AAS88274;
XX DT 13-FEB-2002 (first entry)
DE DNA encoding novel human diagnostic protein #24078.
XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder; ss.
XX Homo sapiens.
OS
XX WO200175067-A2.
PN 11-OCT-2001.
XX 30-MAR-2001; 2001WO-US08631.
XX 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX (HYSE-) HYSEQ INC.
PA Drmanac RT, Liu C, Tang YT;
PI WPTI; 2001-639362/73.
XX

XX (HYSE-) HYSEQ INC.
XX Drmanac RT, Liu C, Tang YT;
XX
XX
XX
XX WPI; 2001-639362/73.
XX P-PSDB; ABG24087.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits and to assess
XX biodiversity
XX
XX Claim 1; SEQ ID No 24078; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. AAS64197-AAS94564 represent novel human
XX diagnostic coding sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
XX Sequence 1533 BP; 362 A; 421 C; 392 G; 358 T; 0 other;
XX
Query Match 100.0%; Score 138; DB 23; Length 1533;
Best Local Similarity 100.0%; Pred. No. 1.3e-33;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGAGCTTGCAGAAATCTGTATGATAGAAATATT 60
Db 1354 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGAGCTTGCAGAAATCTGTATGATAGAAATATT 1413
QY 61 GCTATCGTTTTTGTCTTGTGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 120
Db 1414 GCTATCGTTTTTGTCTTGTGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 1473
QY 121 GACAAGTGTCCTCATGTGC 138
Db 1474 GACAAGTGTCCTCATGTGC 1491
RESULT 6
AAZ48862
ID AAZ48862 standard; cDNA; 1659 BP.
XX
XX AAZ48862;
XX
XX 24-MAR-2000 (first entry)
XX
XX Human XIAP coding sequence.
XX
XX Human; TAB1; XIAP; X-linked inhibitor of apoptosis protein; TGF-beta;
XX transforming growth factor-beta activated kinase 1; monocyte migration;
XX TAK1 binding protein 1; extracellular matrix protein production;
XX cell growth inhibitor; beta-amyloid protein deposition;
XX immunosuppression; transforming growth factor-beta; ds.
XX
XX Homo sapiens.
OS

XX JP11326328-A.
XX
XX 26-NOV-1999.
XX
XX 13-MAY-1998; 98JP-0130378.
XX
XX 13-MAY-1998; 98JP-0130378.
XX (MATSU) MATSUMOTO K.
XX WPI; 2000-078337/07.
XX P-PSDB; AAY59451.
XX
XX Screening a substance which inhibits combination of the X-linked
XX inhibitor of apoptosis protein
XX
XX Disclosure; Page 28-30; 43pp; Japanese.
XX
XX This sequence encodes the human XIAP protein.
XX The invention relates to a method for screening a substance inhibiting
XX the formation of a complex between XIAP and TAB1, in which X-linked
XX inhibitor of apoptosis protein (XIAP), transforming growth factor-beta
XX activated kinase 1(TAK1) binding protein 1(TAB1) and a substance to be
XX tested are contacted with each other and then the presence or formation
XX of a complex between XIAP and TAB1 is detected. The substance can be used
XX as a drug for extracellular matrix protein production enhancement, cell
XX growth inhibition, monocyte migration, physiologically active substance
XX induction, immunosuppression, and beta-amyloid protein deposition. A
XX substance inhibiting the formation of a complex between TAB1 and XIAP as
XX well as between XIAP and TGF-beta (Transforming growth factor-beta) type
XX I and/or type II receptor is useful as a drug.
XX
XX Sequence 1659 BP; 519 A; 296 C; 385 G; 459 T; 0 other;
XX
Query Match 100.0%; Score 138; DB 21; Length 1659;
Best Local Similarity 100.0%; Pred. No. 1.4e-33;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGAGCTTGCAGAAATCTGTATGATAGAAATATT 60
Db 1396 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGAGCTTGCAGAAATCTGTATGATAGAAATATT 1455
QY 61 GCTATCGTTTTTGTCTTGTGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 120
Db 1456 GCTATCGTTTTTGTCTTGTGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 1515
QY 121 GACAAGTGTCCTCATGTGC 138
Db 1516 GACAAGTGTCCTCATGTGC 1533
RESULT 7
AAK99405
ID AAK99405 standard; DNA; 2404 BP.
XX
XX AAK99405;
XX
XX 27-JUN-2002 (first entry)
XX
XX DNA of APP related human homologue hcp35211.
XX
XX Neuroprotective; neurotropic; transgenic fly; Alzheimer's disease; Abeta;
XX amyloid precursor protein; tissue-specific expression control; human APP;
XX APP pathway modulator; gene therapy; gene; ds.
XX
XX Homo sapiens.
XX
XX Location/Qualifiers
XX Key 592..1528
XX CDS /*tag= a
XX /product= "Protein of human homologue hcp35211"
XX /note= "No start codon"

XX WO200226820-A2.
 XX
 XX
 PD 04-APR-2002.
 XX
 XX
 PF 01-OCT-2001; 2001WO-EP11345.
 XX
 PR 29-SEP-2000; 2000US-236893P.
 PR 14-JUN-2001; 2001US-298309P.
 XX
 PA (NOVS.) NOVARTIS AG.
 PA (NOVS.) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 XX Cohen D., Dengler UJ, Finelli AL, Freuler F, Konsolaki M.
 PI Reinhardt MWM, Zusman S,
 XX WPI; 2002-315796/35.
 DR P-PSDB; AAO20511.
 XX
 XX New transgenic fly, containing DNA encoding an Abeta portion of human
 PT APP, useful for identifying agents which modulate the APP pathway and
 PT which can be used to treat Alzheimer's disease -
 XX
 XX Example 4; Page 111; 129pp; English.
 XX
 CC The invention relates to a transgenic fly whose genome comprises DNA
 CC encoding a polypeptide having the Abeta portion of human amyloid
 CC precursor protein (APP), fused to a signal sequence. The DNA sequence
 CC encodes a 123 (Abeta40) or 129 (Abeta42) amino acid sequence, given in
 CC the specification. The DNA sequence is operably linked to a tissue-
 CC specific expression control sequence. Expression of the sequence gives
 CC the fly an altered phenotype. The purpose of the invention is for
 CC identifying agents that inhibit or promote the expression and/or function
 CC of genes or encoded polypeptides which modify the APP pathway. The agent
 CC is a compound, triple helix DNA, antisense oligonucleotide, double
 CC stranded RNA molecule, ribozyme, or particularly an antibody. It is used
 CC to treat conditions such as Alzheimer's disease. The agent can be used as
 CC an APP pathway modulator or in gene therapy. This polynucleotide sequence
 CC represents the DNA of the APP related human homologue hCP35211.
 XX
 SQ Sequence 2404 BP; 759 A; 372 C; 525 G; 748 T; 0 other;
 Query Match 100.0%; Score 136; DB 24; Length 2404;
 Best Local Similarity 100.0%; Pred. No. 1.5e-33;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGGCTTTGCAAAATCTGTATGATAGAAATATT 60
 DB 1349 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGGCTTTGCAAAATCTGTATGATAGAAATATT 1408
 QY 61 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACTTCTTAACAATGCTGTAAGCAGTT 120
 DB 1409 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACTTCTTAACAATGCTGTAAGCAGTT 1468
 QY 121 GACAAGTGTCCCATGTGC 138
 DB 1469 GACAAGTGTCCCATGTGC 1486
 RESULT 8
 AAT70836
 ID AAT70836 standard; cDNA; 2540 BP.
 AC AAT70836;
 XX
 XX 02-SEP-1997 (first entry)
 DT
 XX Human apoptosis inhibitor xiap cDNA.
 DE
 XX Apoptosis inhibitor; X-linked inhibitor of apoptosis protein;
 KW XIAP; HIV; AIDS; neurodegeneration; myelodysplastic syndrome;
 KW ischaemia; myocardial infarction; stroke;
 KW reperfusion injury; toxin-induced liver disease; gene therapy;

KW diagnosis; ds.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 34..1527
 FT /*tag= a
 XX
 XX WO9706255-A2.
 XX
 PD 20-FEB-1997.
 XX
 XX 05-AUG-1996; 96WO-IB01022.
 XX
 XX 22-DEC-1995; 95US-0576956.
 PR 04-AUG-1995; 95US-0511485.
 XX
 XX (UYOT-) UNIV OTTAWA.
 PA
 XX Baird S, Korneluk RG, Liston P, Mackenzie AE;
 XX WPI; 1997-154262/14.
 DR P-PSDB; AAW19581.
 XX
 XX Nucleic acid encoding an inhibitor of apoptosis polypeptide - used
 PT to inhibit apoptosis in e.g. HIV or AIDS patients, and for detection
 PT of susceptibility to apoptotic disease
 XX
 PS Claim 12; Page 67-68; 219pp; English.
 XX
 CC Human xiap, hiap-1 and hiap-2 genes, and murine xiap, hiap-1 and
 CC hiap-2 genes (AAT70836-41) respectively code for a new class of
 CC mammalian proteins (AAW19581-86) that are inhibitors of apoptosis
 CC (IAP). The xiap gene (for X-linked IAP gene) was isolated from a
 CC human foetal brain Zap1 cDNA library using an X-linked sequence
 CC tag site that shows strong homology with the conserved ring zinc
 CC finger domain of baculovirus CpiAP and OpiAP genes. The gene was
 CC assigned to chromosome Xq25 by FISH. IAP nucleic acids can be used
 CC to express IAP polypeptides in cells and animals to inhibit
 CC apoptosis, and as primers and probes to identify and isolate
 CC additional IAP genes, as well as in methods for treating diseases
 CC and disorders involving apoptosis (anti-apoptotic gene therapy).
 XX
 SQ Sequence 2540 BP; 781 A; 415 C; 570 G; 773 T; 1 other;
 Query Match 100.0%; Score 138; DB 18; Length 2540;
 Best Local Similarity 100.0%; Pred. No. 1.5e-33;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGGCTTTGCAAAATCTGTATGATAGAAATATT 60
 DB 1348 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGGCTTTGCAAAATCTGTATGATAGAAATATT 1407
 QY 61 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACTTCTTAACAATGCTGTAAGCAGTT 120
 DB 1408 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACTTCTTAACAATGCTGTAAGCAGTT 1467
 QY 121 GACAAGTGTCCCATGTGC 138
 DB 1468 GACAAGTGTCCCATGTGC 1485
 RESULT 9
 AAA64901
 ID AAA64901 standard; DNA; 2540 BP.
 AC AAA64901;
 XX
 XX 07-NOV-2000 (first entry)
 DT
 XX Human X-linked inhibitor of apoptosis DNA.
 DE
 XX X-linked inhibitor of apoptosis; XIAP; hIAP; MIHA; U45880;
 KW

antisense; antiinflammatory; cytostatic; tumour; ds.

KW

XX Homo sapiens.

XX Location/Qualifiers

XX 34..1527

FT CDS /tag- a

FT /product= "X-linked inhibitor of apoptosis"

XX US6087173-A.

XX 11-JUL-2000.

XX 09-SEP-1999; 99US-0392580.

XX '09-SEP-1999; 99US-0392580.

XX (ISIS-) ISIS PHARM INC.

XX Bennett CF, Cowsett LM, Ackermann EJ;

XX WPI; 2000-498201/44.

XX P-PSDB; AAY99985.

XX Antisense compound useful for research reagents, diagnostics,

XX prophylaxis and for treating disorders associated with X-linked

XX inhibitor of apoptosis, modulates expression of X-linked inhibitor of

XX apoptosis

XX Example 13; Column 43-48; 33pp; English.

XX The present invention relates to antisense oligonucleotides designed to

XX inhibit expression of the human X-linked inhibitor of apoptosis. The

XX present sequence is the X-linked inhibitor of apoptosis DNA.

XX Modified phosphorothioate 2'-methoxyethyl (2'-MOE) oligonucleotides are

XX more effective inhibitors than unmodified oligonucleotides. The

XX oligonucleotides may be used to inhibit X-linked inhibitor of apoptosis

XX expression in cells and tissues in vitro. The oligonucleotides are also

XX useful for treating animals or humans, prone to a disease associated

XX with X-linked inhibitor of apoptosis. The oligonucleotides may also be

XX used prophylactically to prevent infection, inflammation or tumour

XX formation.

XX Sequence 2540 BP; 781 A; 415 C; 571 G; 773 T; 0 other;

XX Query Match 100.0%; Score 138; DB 21; Length 2540;

XX Best Local Similarity 100.0%; Pred. No. 1.5e-33;

XX Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAGGCGCCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 60

DB 1348 GAGCAGCTAGGCGCCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 1407

QY 61 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 120

DB 1408 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 1467

QY 121 GACAAGTGTCCTCATGTGC 138

DB 1468 GACAAGTGTCCTCATGTGC 1485

RESULT 10

ABK93869

ID ABK93869 standard; cDNA; 2540 BP.

XX AC ABK93869;

XX 26-AUG-2002 (first entry)

XX Human cDNA encoding inhibitor of apoptosis, XIAP #1.

XX Human; ss; gene; antisense; inhibitor of apoptosis; XIAP1; XIAP2; XIAP;

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cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;

pancreatic cancer; embryonic development; viral pathogenesis;

autoimmune disorder; neurodegenerative disease; multiple sclerosis;

lupus erythematosus; herpes virus infection; pox virus infection;

adenovirus infection; proliferative disease.

Homo sapiens.

WO200226968-A2.

04-APR-2002.

27-SEP-2001; 2001WO-CA01379.

28-SEP-2000; 2000US-0672717.

(UYOT-) UNIV OTTAWA.

(AEGE-) AEGERA THERAPEUTICS INC.

Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;

WPI; 2002-479562/51.

P-PSDB; ABG65663.

Novel antisense inhibitor of apoptosis nucleic acid useful for

enhancing apoptosis in a cell, for treating cancer and other

proliferative diseases

Disclosure; Fig 1; 135pp; English.

The invention relates to an inhibitor of apoptosis (IAP) antisense

nucleic acid (1) that inhibits IAP biological activity, regardless of

length of the antisense nucleic acid, the IAP proteins may be mouse

or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical

composition comprising a mammalian IAP antisense molecule and a method of

enhancing apoptosis in a cell, comprising administering a negative

regulator of the IAP anti-apoptotic pathway to the cell. The IAP

antisense inhibitor is useful for enhancing apoptosis in a cell in a

mammal diagnosed with a proliferative disease. The method is useful for

treating a patient diagnosed with a proliferative disease like cancer.

The IAP antisense molecule is useful to treat, ameliorate, improve,

sustain or prevent proliferative diseases (e.g. ovarian cancer,

adenocarcinoma, lymphoma, pancreatic cancer,) and also in diseases or

conditions where apoptosis is involved or implicated (e.g. embryonic

development, viral pathogenesis, autoimmune disorders, neurodegenerative

diseases, multiple sclerosis, lupus erythematosus and infection by herpes

virus, pox virus and adenovirus). The present sequence is a human IAP

cDNA sequence.

Sequence 2540 BP; 782 A; 415 C; 549 G; 772 T; 22 other;

Query Match 100.0%; Score 138; DB 24; Length 2540;

Best Local Similarity 100.0%; Pred. No. 1.5e-33;

Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAGGCGCCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 60

DB 1348 GAGCAGCTAGGCGCCTGCAAGAGGAGAGCTTGGCAAAATCTGTATGGATAGAAATATT 1407

QY 61 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 120

DB 1408 GCTATCGTTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGCTGCTGAAGCAGTT 1467

QY 121 GACAAGTGTCCTCATGTGC 138

DB 1468 GACAAGTGTCCTCATGTGC 1485

RESULT 11

ABK93875

ID ABK93875 standard; cDNA; 3000 BP.

XX AC ABK93875;

XX 26-AUG-2002 (first entry)
XX Human cDNA encoding inhibitor of apoptosis, XIAP #2.
XX Human; ss; gene; antisense; inhibitor of apoptosis; HIAP1; HIAP2; XIAP;
KW cytostatic; cancer; ovarian cancer; adenocarcinoma; lymphoma; IAP;
KW pancreatic cancer; embryonic development; viral pathogenesis;
KW autoimmune disorder; neurodegenerative disease; multiple sclerosis;
KW lupus erythematosus; herpes virus infection; pox virus infection;
KW adenovirus infection; proliferative disease.
XX Homo sapiens.
XX WO200226968-A2.
XX 04-APR-2002.
XX 27-SEP-2001; 2001WO-CA01379.
XX 28-SEP-2000; 2000US-0672717.
XX (UYOT-) UNIV OTTAWA.
XX (AEGE-) AEGERA THERAPEUTICS INC.
XX Korneluk RG, Lacasse E, Baird S, Holcik M, Young S;
XX WPI; 2002-479562/51.
XX Novel antisense inhibitor of apoptosis nucleic acid useful for
PT enhancing apoptosis in a cell, for treating cancer and other
PT proliferative diseases
XX Example 2; Fig 15; 135pp; English.
XX The invention relates to an inhibitor of apoptosis (IAP) antisense
CC nucleic acid (I) that inhibits IAP biological activity, regardless of
CC length of the antisense nucleic acid, the IAP proteins may be mouse
CC or human XIAP, HIAP1 or HIAP2. Also included are a pharmaceutical
CC composition comprising a mammalian IAP antisense molecule and a method of
CC enhancing apoptosis in a cell, comprising administering a negative
CC regulator of the IAP anti-apoptotic pathway to the cell. The IAP
CC antisense inhibitor is useful for enhancing apoptosis in a cell in a
CC mammal diagnosed with a proliferative disease. The method is useful for
CC treating a patient diagnosed with a proliferative disease like cancer.
CC The IAP antisense molecule is useful to treat, ameliorate, improve,
CC sustain or prevent proliferative diseases (e.g. ovarian cancer,
CC adenocarcinoma, lymphoma, pancreatic cancer.) and also in diseases or
CC conditions where apoptosis is involved or implicated (e.g. embryonic
CC development, viral pathogenesis, autoimmune disorders, neurodegenerative
CC diseases, multiple sclerosis, lupus erythematosus and infection by herpes
CC virus, pox virus and adenovirus). The present sequence is a human IAP
CC cDNA sequence.
XX SQ Sequence 3000 BP; 974 A; 452 C; 601 G; 973 T; 0 other;
Query Match 100.0%; Score 138; DB 24; Length 3000;
Best Local Similarity 100.0%; Pred. No. 1.6e-33;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
DB 2004 GAGCAGCTAAGGCGCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 2063
QY 61 GCTATCGTTTTTGTCTGTGACATCTAGTCACCTGTGTAACAATGCTGTAAGCAGTT 120
DB 2064 GCTATCGTTTTTGTCTGTGACATCTAGTCACCTGTGTAACAATGCTGTAAGCAGTT 2123
QY 121 GACAAGTGCCCATGTGC 138
DB 2124 GACAAGTGCCCATGTGC 2141

RESULT 12
AAV5038
ID AAV5038 standard; cDNA; 5232 BP.
XX AC AAV5038;
XX 13-NOV-1998 (first entry)
XX Human XIAP coding sequence.
XX Inhibitor of apoptosis protein; apoptosis enhancer; NAIP polypeptide;
KW proliferative disease; IAP; therapy; cancer; human; XIAP protein; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
FH 34..1527
FT /*tag= a
FT /product= XIAP
XX WO9835693-A2.
XX 20-AUG-1998.
XX 13-FEB-1998; 98WO-IB00781.
XX 13-FEB-1997; 97US-0800929.
XX (UYOT-) UNIV OTTAWA.
XX Baird S, Korneluk R, Liston P, Mackenzie AE, Pratt C;
PI Tsang B;
XX WPI; 1998-467164/40.
XX P-PSDB; AAW69294.
XX Inducing apoptosis in proliferative mammalian cells with inhibitor
PT of IAP or NAIP polypeptide - also methods for prognosis based on
PT presence of IAP and NAIP, specifically applied to cancers involving
PT p53 mutations
XX Claim 13; Fig 1; 147pp; English.
XX This sequence encodes the human XIAP protein, which is an inhibitor of
CC apoptosis protein (IAP), and can be used in the method of the invention.
CC The method is for enhancing apoptosis in cells from a mammal with
CC proliferative disease by treatment with a compound that inhibits
CC biological activity of an IAP or NAIP polypeptide. The inhibitory
CC compounds are used to treat proliferative diseases, specially cancers of
CC ovary, breast, pancreas, lymph nodes, skin, blood, lung, brain, kidney,
CC liver, nasopharynx, thyroid, central nervous system, prostate, colon,
CC rectum, cervix or endometrium, particularly to increase their sensitivity
CC to chemotherapeutic agents. High levels of the IAP or NAIP proteins are
CC detected in many cancers and are associated with poor prognosis,
CC resistance to chemotherapeutic agents and mutations in p53 (it is
CC suggested that wild-type p53 suppresses transcription of the IAP or NAIP
CC genes). Transgenic animals are used for testing the effects of antisense
CC oligonucleotides and for screening for the inhibitors.
XX SQ Sequence 5232 BP; 1579 A; 861 C; 1062 G; 1728 T; 2 other;
Query Match 100.0%; Score 138; DB 19; Length 5232;
Best Local Similarity 100.0%; Pred. No. 1.9e-33;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
DB 1348 GAGCAGCTAAGGCGCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 1407
QY 61 GCTATCGTTTTTGTCTGTGACATCTAGTCACCTGTGTAACAATGCTGTAAGCAGTT 120
DB 1408 GCTATCGTTTTTGTCTGTGACATCTAGTCACCTGTGTAACAATGCTGTAAGCAGTT 1467

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QY 121 GACAACTGCCCCATGTC 138
      |||||
DB 1468 GACAACTGCCCCATGTC 1485
      |||||

RESULT 13
ABA48694/c
ID ABA48694 standard; DNA; 148 BP.
XX ABA48694;
AC ABA48694;
DT 01-FEB-2002 (first entry)
XX Human breast cell single exon nucleic acid probe #7389.
DE Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer; ss.
XX Homo sapiens.
OS WO200157271-A2.
PN 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00662.
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-496933/54.
XX New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX Claim 4; SEQ ID NO 7389; 327pp + sequence listing; English.
XX The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and Bt 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids
CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC encode proteins, they are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present invention is a single exon nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 148 BP; 43 A; 36 C; 25 G; 44 T; 0 other;
      Query Match 97.1%; Score 134; DB 22; Length 148;
      Best Local Similarity 100.0%; Pred. No. 1.2e-32;
      Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGATAGAAATATT 60
      |||||
DB 134 GAGCAGCTAAGGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGATAGAAATATT 75
      |||||
QY 61 GCTATCGTTTGTCTTCTGTCACATCTAGTCACCTTTGAAACAATGCTGCTGAAGCAGTT 120
      |||||
DB 74 GCTATCGTTTGTCTTCTGTCACATCTAGTCACCTTTGAAACAATGCTGCTGAAGCAGTT 15
      |||||
QY 121 GACAACTGCCCCAT 134
      |||||
DB 14 GACAACTGCCCCAT 1
      |||||

RESULT 14
AAI21530/c
ID AAI21530 standard; DNA; 148 BP.
XX AAI21530;
AC AAI21530;
DT 12-OCT-2001 (first entry)
XX Probe #11463 for gene expression analysis in human cervical cell sample.
DE Probe; human; microarray; gene expression; cervical epithelial cell;
KW cervical cancer; ss.
XX Homo sapiens.
OS WO200157278-A2.
PN 09-AUG-2001.
XX 30-JAN-2001; 2001WO-US00670.
XX 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX (MOLE-) MOLECULAR DYNAMICS INC.
PA Penn SG, Hanzel DK, Chen W, Rank DR;
PI WPI; 2001-488901/53.
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX Claim 25; SEQ ID NO 11463; 487pp; English.
XX The present invention relates to human single exon nucleic acid probes
CC (SENPs). The present sequence is one such probe. The SENPs are derived
CC from human HeLa cells. The SENPs can be used to produce a single exon
CC microarray, which can be used for measuring human gene expression in a
CC sample derived from human cervical epithelial cells. By measuring gene
CC expression, the probes are therefore useful in grading and/or staging
CC of diseases of the cervix, notably cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX SQ Sequence 148 BP; 43 A; 36 C; 25 G; 44 T; 0 other;
      Query Match 97.1%; Score 134; DB 22; Length 148;
      Best Local Similarity 100.0%; Pred. No. 1.2e-32;
      Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGATAGAAATATT 60
      |||||
DB 134 GAGCAGCTAAGGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGATAGAAATATT 75
      |||||
QY 61 GCTATCGTTTGTCTTCTGTCACATCTAGTCACCTTTGAAACAATGCTGCTGAAGCAGTT 120
      |||||
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Db	74	GCTATCGTTTTTTTCTTGGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT	15
QY	121	GACAAGTGTCCTCAT	134
Db	14	GACAAGTGTCCTCAT	1

Search completed: April 15, 2003, 21:45:30
Job time : 93.2396 secs

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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:16:42 ; Search time 17.3698 Seconds
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2436.494 Million cell updates/sec

Title: US-09-654-743-48
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 441362 seqs, 153338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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5: /cgn2.6/prodata/1/ina/PCUTUS_COMB.seq.*
6: /cgn2.6/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	138	100.0	1588	4	US-09-239-867-3
2	138	100.0	2540	2	US-08-511-485-3
3	138	100.0	2540	3	US-09-392-580-1
4	138	100.0	5232	3	US-09-212-971-3
5	138	100.0	5232	3	US-08-800-929A-3
6	138	100.0	5232	4	US-09-617-053A-3
7	125.2	90.7	2100	2	US-08-511-485-9
8	125.2	90.7	2691	3	US-09-212-971-9
9	125.2	90.7	2691	3	US-08-800-929A-9
10	125.2	90.7	2691	4	US-09-617-053A-9
11	119.4	86.5	152331	3	US-09-128-155-16
12	119.4	86.5	176373	3	US-09-128-155-17
13	117.2	84.9	711	3	US-09-121-979-3
14	117.2	84.9	711	3	US-09-332-319-3
15	117.2	84.9	1529	4	US-09-239-867-1
16	61.2	44.3	2862	4	US-08-569-749-13
17	61.2	44.3	2862	5	PCT-US96-12860-13
18	61.2	44.3	3151	3	US-09-212-971-13
19	61.2	44.3	3151	3	US-08-800-929A-13
20	61.2	44.3	3151	4	US-09-617-053A-13
21	58.6	42.5	2601	4	US-08-569-749-3
22	58.6	42.5	2601	5	PCT-US96-12860-3
23	58.6	42.5	2676	3	US-09-212-971-11
24	58.6	42.5	2676	3	US-08-800-929A-11
25	58.6	42.5	2676	4	US-09-617-053A-11
26	58.6	42.5	3076	2	US-09-205-144-1
27	58.6	42.5	6669	3	US-09-212-971-5

28 58.6 42.5 6669 3 US-08-800-929A-5
29 58.6 42.5 6669 4 US-09-617-053A-5
30 57 41.3 2676 2 US-08-511-485-5
31 54.8 39.7 1435 5 PCT-US95-05922A-1
32 54.8 39.7 2580 2 US-08-511-485-7
33 54.8 39.7 2589 4 US-08-569-749-1
34 54.8 39.7 2589 5 PCT-US96-12860-1
35 54.8 39.7 3532 2 US-09-205-204-1
36 54.8 39.7 3532 3 US-09-212-971-7
37 54.8 39.7 3732 3 US-08-800-929A-7
38 54.8 39.7 3732 4 US-09-617-053A-7
39 32.4 23.5 2169 4 US-09-434-408-3
40 32 23.2 2026 4 US-09-324-455-1
41 32 23.2 2026 4 US-09-324-455-3
42 30.2 21.9 360 3 US-08-935-263-17
43 30.2 21.9 360 4 US-09-594-185-17
44 30.2 21.9 1875 1 US-08-286-325A-1
45 30.2 21.9 3234 1 US-08-286-325A-7

ALIGNMENTS

RESULT 1
US-09-239-867-3
; Sequence 3, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; PRIOR FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 1588
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-239-867-3

Query Match 100.0%; Score 138; DB 4; Length 1588;
Best Local Similarity 100.0%; Pred. No. 3.7e-37;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGGAGCTTGGCAAAATCTGTATGGATAGAAATATT 60
Db 1348 GAGCAGCTAAGCGCGCTGCAAGAGGAGAGGAGCTTGGCAAAATCTGTATGGATAGAAATATT 1407
QY 61 GCTATCGTTTTGTTCCTTGTGGACATCTAGTCACTTCTTAACAATGCTGCTGAAGCAGATT 120
Db 1408 GCTATCGTTTTGTTCCTTGTGGACATCTAGTCACTTCTTAACAATGCTGCTGAAGCAGATT 1467
QY 121 GACAAGTGTCCCATGTGC 138
Db 1468 GACAAGTGTCCCATGTGC 1485

RESULT 2
US-08-511-485-3
; Sequence 3, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:


```

RESULT 3
US-09-392-580-1
; Sequence 1, Application US/09392580
; Patent No. 6087173
; GENERAL INFORMATION:
; APPLICANT: C. Frank Bennett
; APPLICANT: Elizabeth J. Ackermann
; APPLICANT: Lex M. Cowser
; TITLE OF INVENTION: ANTISENSE MODULATION OF X-LINKED INHIBITOR OF APOPTOSIS EXPRESSED
; FILE REFERENCE: RTS-0072
; CURRENT APPLICATION NUMBER: US/09/392,580
; CURRENT FILING DATE: 1999-09-09
; NUMBER OF SEQ ID NOS: 47
; SEQ ID NO 1
; LENGTH: 2540
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (34)..(1527)
US-09-392-580-1

Query Match          Score 138; DB 3; Length 2540;
Best Local Similarity 100.0%; Pred. NO. 4.4e-37;

```

[illegible]

Sequence 3, Application US/08800929A
Patent No. 6133437
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF
TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/800,929A
FILING DATE: 13-FEB-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/030,590
FILING DATE: 14-NOV-1996
APPLICATION NUMBER: 60/017,354
FILING DATE: 28-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Bieker-Brady, Kristina
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 07891/009001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5232 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: Other
LOCATION: 1...5232
OTHER INFORMATION: N at 4622 and 4633 can be A, G, T or C.

Query Match 100.0%; Score 138; DB 3; Length 5232;
Best Local Similarity 100.0%; Pred. No. 5.7e-37;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGGCCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
|||||
Db 1348 GAGCAGCTAAGGGCCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 1407
QY 61 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 120
|||||
Db 1408 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 1467

QY 121 GACAAGTGTCCTCATGTGC 138
|||||
Db 1468 GACAAGTGTCCTCATGTGC 1485

RESULT 6

US-09-617-053A-3
Sequence 3, Application US/09617053A
Patent No. 6300492
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G
APPLICANT: Mackenzie, Alexander E
APPLICANT: Liston, Peter
APPLICANT: Baird, Stephen
APPLICANT: Tsang, Benjamin K
APPLICANT: Pratt, Christine
TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
TITLE OF INVENTION: DISEASE
FILE REFERENCE: 07891/009003
CURRENT APPLICATION NUMBER: US/09/617,053A
CURRENT FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: US 08/800,929
PRIOR FILING DATE: 1997-02-13
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 5232
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: variation
LOCATION: (4623)...(4623)
OTHER INFORMATION: n can be any nucleotide
NAME/KEY: variation
LOCATION: (4622)...(4622)
OTHER INFORMATION: n can be any nucleotide
US-09-617-053A-3
Query Match 100.0%; Score 138; DB 4; Length 5232;
Best Local Similarity 100.0%; Pred. No. 5.7e-37;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 GAGCAGCTAAGGGCCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
|||||
Db 1348 GAGCAGCTAAGGGCCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 1407
QY 61 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 120
|||||
Db 1408 GCTATCGTTTTTGTCTTGTGGACATCTAGTCACTTGTAAACAATGTGCTGAAGCAGTT 1467
QY 121 GACAAGTGTCCTCATGTGC 138
|||||
Db 1468 GACAAGTGTCCTCATGTGC 1485
RESULT 7
US-08-511-485-9
Sequence 9, Application US/08511485
Patent No. 5915912
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/511,485
;; FILING DATE: 04-AUG-1995
;; CLASSIFICATION: 514
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Clark, Paul T.
;; REGISTRATION NUMBER: 30,162
;; REFERENCE/DOCKET NUMBER: 07540/002001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617/542-5070
;; TELEFAX: 617/542-8906
;; TELEX: 200154
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2100 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: both
;; TOPOLOGY: both
;; MOLECULE TYPE: DNA (genomic)
US-08-511-485-9

Query Match 90.7%; Score 125.2; DB 2; Length 2100;
Best Local Similarity 94.2%; Pred. No. 8.2e-33;
Matches 130; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
DB 1438 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 1497

QY 61 GCTATCGTTTTTCTTCTGTGGACATCTAGTCACATTTGTAACAATGTCTGAAGCAGTT 120
DB 1498 GCTATCGTTTTTCTTCTGTGGACATCTAGTCACATTTGTAACAATGTCTGAAGCAGTT 1557

QY 121 GACAAGTGTCCCATGTGC 138
DB 1558 GACAAATGTCCCATGTGC 1575

RESULT 8
US-09-212-971-9
;; Sequence 9, Application US/09212971B
;; Patent No. 6107041
;; GENERAL INFORMATION:
;; APPLICANT: Korneluk, Robert G
;; APPLICANT: Mackenzie, Alexander E
;; APPLICANT: Liston, Peter
;; APPLICANT: Baird, Stephen
;; APPLICANT: Tsang, Benjamin K
;; APPLICANT: Pratt, Christine
;; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
;; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
;; FILE REFERENCE: 07891/009002
;; CURRENT APPLICATION NUMBER: US/09/212,971B
;; CURRENT FILING DATE: 1998-12-16
;; EARLIER APPLICATION NUMBER: 60/017,354
;; EARLIER FILING DATE: 1996-04-26
;; EARLIER APPLICATION NUMBER: 60/030,590
;; EARLIER FILING DATE: 1996-11-14
;; EARLIER APPLICATION NUMBER: 08/800,929
;; EARLIER FILING DATE: 1997-02-13
;; NUMBER OF SEQ ID NOS: 17
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 9
;; LENGTH: 2691
;; TYPE: DNA
;; ORGANISM: Mus musculus
US-09-212-971-9

Query Match 90.7%; Score 125.2; DB 3; Length 2691;
Best Local Similarity 94.2%; Pred. No. 8.9e-33;
Matches 130; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
DB 1983 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 2042

QY 61 GCTATCGTTTTTCTTCTGTGGACATCTAGTCACATTTGTAACAATGTCTGAAGCAGTT 120
DB 2043 GCTATCGTTTTTCTTCTGTGGACATCTAGTCACATTTGTAACAATGTCTGAAGCAGTT 2102

QY 121 GACAAGTGTCCCATGTGC 138
DB 2103 GACAAATGTCCCATGTGC 2120

RESULT 9
US-08-800-929A-9
;; Sequence 9, Application US/08800929A
;; Patent No. 6133437
;; GENERAL INFORMATION:
;; APPLICANT: Korneluk, Robert G
;; APPLICANT: Mackenzie, Alexander E
;; APPLICANT: Liston, Peter
;; APPLICANT: Baird, Stephen
;; APPLICANT: Tsang, Benjamin K
;; APPLICANT: Pratt, Christine
;; TITLE OF INVENTION: DETECTION AND MODULATION OF
;; TITLE OF INVENTION: IAPS AND NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERAT
;; NUMBER OF SEQUENCES: 17
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Clark & Eibing LLP
;; STREET: 176 Federal Street
;; CITY: Boston
;; STATE: MA
;; COUNTRY: USA
;; ZIP: 02110
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Diskette
;; COMPUTER: IBM Compatible
;; OPERATING SYSTEM: DOS
;; SOFTWARE: FastSeq for Windows Version 2.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/800,929A
;; FILING DATE: 13-FEB-1997
;; CLASSIFICATION: 424
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 60/030,590
;; FILING DATE: 14-NOV-1996
;; APPLICATION NUMBER: 60/017,354
;; FILING DATE: 26-APR-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Bieker-Brady, Kristina
;; REGISTRATION NUMBER:
;; REFERENCE/DOCKET NUMBER: 07891/009001
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 617-428-0200
;; TELEFAX: 617-428-7045
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 2691 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cdna
US-08-800-929A-9

Query Match 90.7%; Score 125.2; DB 3; Length 2691;
Best Local Similarity 94.2%; Pred. No. 8.9e-33;
Matches 130; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
DB 1983 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 2042

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QY 61 GCTATCGTTTGTTCCTTGGACATCTAGTCACCTGTAAACAAATGCTGAAGCAGTT 120
|||||
Db 2043 GCTATCGTTTGTTCCTTGGACATCTAGTCACCTGTAAACAAATGCTGAAGCAGTT 2102
|||||
QY 121 GACAAGTGCCCATGTGC 138
|||||
Db 2103 GACAAGTGCCCATGTGC 2120
|||||

RESULT 10
US-09-617-053A-9
; Sequence 9, Application US/09617053A
; Patent No. 6300492
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF TAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009003
; CURRENT APPLICATION NUMBER: US/09/617,053A
; CURRENT FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-617-053A-9

Query Match 90.7%; Score 125.2; DB 4; Length 2691;
Best Local Similarity 94.2%; Pred. No. 8.9e-33;
Matches 130; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
|||||
Db 1983 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 2042
|||||

QY 61 GCTATCGTTTGTTCCTTGTGACATCTAGTCACCTGTAAACAAATGCTGAAGCAGTT 120
|||||
Db 2043 GCTATCGTTTGTTCCTTGTGACATCTAGTCACCTGTAAACAAATGCTGAAGCAGTT 2102
|||||

QY 121 GACAAGTGCCCATGTGC 138
|||||
Db 2103 GACAAGTGCCCATGTGC 2120
|||||

RESULT 11
US-09-128-155-16/c
; Sequence 16, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16/c

Query Match 86.5%; Score 119.4; DB 3; Length 152331;
Best Local Similarity 92.0%; Pred. No. 3.3e-30;
Matches 126; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
|||||
Db 13011 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 13070
|||||

QY 61 GCTATCGTTTGTTCCTTGTGACATCTAGTCACCTGTAAACAAATGCTGAAGCAGTT 120
|||||
Db 13071 GCTATCGTTTGTTCCTTGTGACATCTAGTCACCTGTAAACAAATGCTGAAGCAGTT 13130
|||||

QY 121 GACAAGTGCCCATGTGC 137
|||||
Db 13131 GACAAGTGCCCATGTGC 13147
|||||

RESULT 13
US-09-121-979-3
; Sequence 3, Application US/09121979
; Patent No. 6159709
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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-16

Query Match 86.5%; Score 119.4; DB 3; Length 152331;
Best Local Similarity 92.0%; Pred. No. 3.3e-30;
Matches 126; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
|||||
Db 24123 GAGCAGCTAAGCACCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 24064
|||||

QY 61 GCTATCGTTTGTTCCTTGTGACATCTAGTCACCTGTAAACAAATGCTGAAGCAGTT 120
|||||
Db 24063 GCTATCGTTTGTTCCTTGTGACATCTAGTCACCTGTAAACAAATGCTGAAGCAGTT 24004
|||||

QY 121 GACAAGTGCCCATGTGC 137
|||||
Db 24003 GACAAGTGCTCAAGTG 23987
|||||

RESULT 12
US-09-128-155-17
; Sequence 17, Application US/09128155
; Patent No. 6117654
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/09/128,155
; CURRENT FILING DATE: 1998-08-03
; EARLIER APPLICATION NUMBER: US 60/091,650
; EARLIER FILING DATE: 1998-07-02
; EARLIER APPLICATION NUMBER: US 60/054,646
; EARLIER FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; NAME/KEY: misc_feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-09-128-155-17

Query Match 86.5%; Score 119.4; DB 3; Length 176373;
Best Local Similarity 92.0%; Pred. No. 3.5e-30;
Matches 126; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
|||||
Db 13011 GAGCAGCTAAGCACCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 13070
|||||

QY 61 GCTATCGTTTGTTCCTTGTGACATCTAGTCACCTGTAAACAAATGCTGAAGCAGTT 120
|||||
Db 13071 GCTATCGTTTGTTCCTTGTGACATCTAGTCACCTGTAAACAAATGCTGAAGCAGTT 13130
|||||

QY 121 GACAAGTGCCCATGTGC 137
|||||
Db 13131 GACAAGTGCTCAAGTG 13147
|||||

RESULT 13
US-09-121-979-3
; Sequence 3, Application US/09121979
; Patent No. 6159709
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```

; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021001
; CURRENT APPLICATION NUMBER: US/09/121,979
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-121-979-3

Query Match      84.9%; Score 117.2; DB 3; Length 711;
Best Local Similarity 90.6%; Pred. No. 2.7e-30;
Matches 125; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 532 GAGCCGCTAAGCGCTGCAAGAGGAGAGCTTTGTAATAATCTGCATGGACAGATATATC 591

QY 61 GCTATCGTTTTTCTTCTGTGACATCTAGTCACCTGTGTAACAATGTGCTGAAGCAGTT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 592 GCTGTTGTTTTTATTCCTTGTGACATCTGGTCACCTGTGTAACAATGTGCTGAAGCAGTT 651

QY 121 GACAAGTGTCCTCATGTGC 138
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 652 GACAGATGTCCTCATGTGC 669

RESULT 14
US-09-332-319-3
; Sequence 3, Application US/09332319
; Patent No. 6171821
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Holcik, Martin
; APPLICANT: Liston, Peter
; TITLE OF INVENTION: XIAP IRES AND USES THEREOF
; FILE REFERENCE: 07891/021002
; CURRENT APPLICATION NUMBER: US/09/332,319
; CURRENT FILING DATE: 1999-06-14
; EARLIER APPLICATION NUMBER: 09/121,979
; EARLIER FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 711
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-332-319-3

Query Match      84.9%; Score 117.2; DB 4; Length 711;
Best Local Similarity 90.6%; Pred. No. 2.7e-30;
Matches 125; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 532 GAGCCGCTAAGCGCTGCAAGAGGAGAGCTTTGTAATAATCTGCATGGACAGATATATC 591

QY 61 GCTATCGTTTTTCTTCTGTGACATCTAGTCACCTGTGTAACAATGTGCTGAAGCAGTT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 592 GCTGTTGTTTTTATTCCTTGTGACATCTGGTCACCTGTGTAACAATGTGCTGAAGCAGTT 651

QY 121 GACAAGTGTCCTCATGTGC 138
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 652 GACAGATGTCCTCATGTGC 669

RESULT 15
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US-09-239-867-1
; Sequence 1, Application US/09239867
; Patent No. 6331412
; GENERAL INFORMATION:
; APPLICANT: Robert G. Korneluk et al.
; TITLE OF INVENTION: METHODS AND COMPOUNDS FOR MODULATING
; TITLE OF INVENTION: MALE FERTILITY
; FILE REFERENCE: 07891/018002
; CURRENT APPLICATION NUMBER: US/09/239,867
; CURRENT FILING DATE: 1999-01-29
; PRIOR APPLICATION NUMBER: 60/073,001
; PRIOR FILING DATE: 1998-01-29
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1559
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)-(1559)
; OTHER INFORMATION: n = A,T,C or G
US-09-239-867-1

Query Match      84.9%; Score 117.2; DB 4; Length 1559;
Best Local Similarity 90.6%; Pred. No. 3.6e-30;
Matches 125; Conservative 0; Mismatches 13; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1322 GAGCCGCTAAGCGCTGCAAGAGGAGAGCTTTGTAATAATCTGCATGGACAGATATATC 1381

QY 61 GCTATCGTTTTTCTTCTGTGACATCTAGTCACCTGTGTAACAATGTGCTGAAGCAGTT 120
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1382 GCTGTTGTTTTTATTCCTTGTGACATCTGGTCACCTGTGTAACAATGTGCTGAAGCAGTT 1441

QY 121 GACAAGTGTCCTCATGTGC 138
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1442 GACAGATGTCCTCATGTGC 1459

Search completed: April 16, 2003, 00:58:51
Job time : 54.3698 secs
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: April 15, 2003, 21:33:02 ; Search time 33.1823 Seconds
(without alignments)
3648.005 Million cell updates/sec

Title: US-09-654-743-48
Perfect score: 138
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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 593429 seqs, 438583890 residues
Total number of hits satisfying chosen parameters: 1186858

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications, NA.*

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11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq.*
12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq.*
13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq.*
14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	138	100.0	2540	9	US-09-201-936-3
4	138	100.0	5232	10	US-09-974-592-3
5	134	97.1	148	10	US-09-864-761-30419
6	125.2	90.7	2100	9	US-09-201-936-9
7	125.2	90.7	2691	10	US-09-974-592-9
8	119.4	86.5	152331	9	US-10-095-407-16
9	119.4	86.5	176373	9	US-10-095-407-17
10	61.2	44.3	2416	9	US-09-201-936-41
11	61.2	44.3	3151	10	US-09-974-592-13
12	60.2	43.6	2450	9	US-09-201-936-39
13	58.6	42.5	2676	10	US-09-974-592-11
14	58.6	42.5	3076	9	US-09-954-531-16
15	58.6	42.5	3076	10	US-09-954-456-1635
16	58.6	42.5	6669	10	US-09-974-592-5
17	57	41.3	460	10	US-09-960-352-8049
18	57	41.3	2676	9	US-09-201-936-5
19	54.8	39.7	2580	9	US-09-201-936-7

20	54.8	39.7	3532	10	US-09-880-107-3354
21	54.8	39.7	3732	10	US-09-974-592-7
C 22	33	23.9	456	10	US-09-770-444-524
23	32	23.2	1992	9	US-09-949-842-2
C 24	32	23.2	8847	9	US-10-092-154-995
C 25	32	23.2	8847	10	US-09-764-847-995
26	30.2	21.9	360	12	US-10-033-078-17
27	29.6	21.4	9139	10	US-09-965-553-22
28	29.2	21.2	5744	10	US-09-764-877-3507
C 29	28.8	20.9	32193	9	US-09-764-868-1508
30	28.8	20.9	98865	10	US-09-770-689A-3
31	28.8	20.9	173808	12	US-10-003-806-10
32	28.6	20.7	629	10	US-09-917-800A-885
C 33	28.6	20.7	197496	9	US-09-877-177-10
C 34	28.4	20.6	336	10	US-09-960-352-9169
35	28.4	20.6	4232	10	US-09-070-927A-71
C 36	28.2	20.4	924	9	US-09-738-626-769
C 37	28.2	20.4	3309400	9	US-09-738-626-1
C 38	28	20.3	306	9	US-09-796-692-4055
C 39	28	20.3	368004	10	US-09-949-654-3
C 40	27.8	20.1	2127	10	US-09-974-300-1668
41	27.6	20.0	1023	9	US-09-938-842A-2411
42	27.6	20.0	2811	9	US-09-938-842A-2538
43	27.6	20.0	6417	10	US-09-764-877-3505
C 44	27.6	20.0	20165	9	US-10-199-330-7
C 45	27.6	20.0	20165	9	US-10-199-334-7

ALIGNMENTS

RESULT 1

US-09-864-761-13853/c
; Sequence 13853, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30

;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 13853
;; LENGTH: 489
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AL022156.1
;; OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 1.1
;; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2.1
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1
;; OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.8
US-09-864-761-13853

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Best Local Similarity 100.0%; Pred. No. 4.6e-35;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
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DB 450 GAGCAGCTAAGGCGCTGCAAGAGGAGAGGAGCTTTGCAAAATCTGTATGGATAGAAATATT 391
|||||
QY 61 GCTATCGTTTTTGTCTTCTGACATCTAGTCACCTTTGTAACAATGTGCTGAAGCAGTT 120
|||||
DB 390 GCTATCGTTTTTGTCTTCTGACATCTAGTCACCTTTGTAACAATGTGCTGAAGCAGTT 331
|||||
QY 121 GACAAGTGTCCTCATGTGC 138
|||||
DB 330 GACAAGTGTCCTCATGTGC 313
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RESULT 2
US-09-964-899-38
;; Sequence 38, Application US/09964899
;; Patent No. US20020174446A1
;; GENERAL INFORMATION:
;; APPLICANT: Cohen, Dalia et al.
;; TITLE OF INVENTION: Identification of Genes Involved in
;; TITLE OF INVENTION: Alzheimer's Disease Using Drosophila Melanogaster
;; FILE REFERENCE: 4-31612 A
;; CURRENT APPLICATION NUMBER: US/09/964,899
;; PRIOR FILING DATE: 2001-09-27
;; PRIOR APPLICATION NUMBER: 60/236,893
;; PRIOR FILING DATE: 2000-09-29
;; PRIOR APPLICATION NUMBER: 60/298,309
;; PRIOR FILING DATE: 2001-06-14
;; NUMBER OF SEQ ID NOS: 53
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 38
;; LENGTH: 2404
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-09-964-899-38

Query Match 100.0%; Score 138; DB 9; Length 2404;
Best Local Similarity 100.0%; Pred. No. 9.6e-35;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
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DB 1349 GAGCAGCTAAGGCGCTGCAAGAGGAGAGGAGCTTTGCAAAATCTGTATGGATAGAAATATT 1408
|||||
QY 61 GCTATCGTTTTTGTCTTCTGACATCTAGTCACCTTTGTAACAATGTGCTGAAGCAGTT 120
|||||
DB 1409 GCTATCGTTTTTGTCTTCTGACATCTAGTCACCTTTGTAACAATGTGCTGAAGCAGTT 1468
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QY 121 GACAAGTGTCCTCATGTGC 138
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DB 1469 GACAAGTGTCCTCATGTGC 1486
|||||

RESULT 3
US-09-201-936-3
;; Sequence 3, Application US/09201936
;; Publication No. US20020187946A1
;; GENERAL INFORMATION:
;; APPLICANT: Korneluk, Robert G.
;; APPLICANT: Mackenzie, Alexander E.
;; APPLICANT: Baird, Stephen
;; APPLICANT: Liston, Peter
;; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
;; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
;; FILE REFERENCE: 07891/003003
;; CURRENT APPLICATION NUMBER: US/09/201,936
;; CURRENT FILING DATE: 1998-12-01
;; EARLIER APPLICATION NUMBER: 09/011,356
;; EARLIER FILING DATE: 1998-02-04
;; EARLIER APPLICATION NUMBER: PCT/IB96/01022
;; EARLIER FILING DATE: 1996-08-05
;; EARLIER APPLICATION NUMBER: 08/576,956
;; EARLIER FILING DATE: 1995-12-22
;; EARLIER APPLICATION NUMBER: 08/511,485
;; EARLIER FILING DATE: 1995-08-04
;; NUMBER OF SEQ ID NOS: 45
;; SOFTWARE: FastSeq for Windows Version 3.0
;; SEQ ID NO 3
;; LENGTH: 2540
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; NAME/KEY: variation
;; LOCATION: (2540)....(2540)
;; OTHER INFORMATION: N may be any nucleotide
US-09-201-936-3

Query Match 100.0%; Score 138; DB 9; Length 2540;
Best Local Similarity 100.0%; Pred. No. 9.8e-35;
Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
|||||
DB 1348 GAGCAGCTAAGGCGCTGCAAGAGGAGAGGAGCTTTGCAAAATCTGTATGGATAGAAATATT 1407
|||||
QY 61 GCTATCGTTTTTGTCTTCTGACATCTAGTCACCTTTGTAACAATGTGCTGAAGCAGTT 120
|||||
DB 1408 GCTATCGTTTTTGTCTTCTGACATCTAGTCACCTTTGTAACAATGTGCTGAAGCAGTT 1467
|||||

QY 121 GACAAGTGTCCTCATGTGC 138
|||||
DB 1468 GACAAGTGTCCTCATGTGC 1485
|||||

RESULT 4
US-09-974-592-3
;; Sequence 3, Application US/09974592
;; Patent No. US20020120121A1
;; GENERAL INFORMATION:
;; APPLICANT: Korneluk, Robert G.
;; APPLICANT: Mackenzie, Alexander E.
;; APPLICANT: Liston, Peter
;; APPLICANT: Baird, Stephen
;; APPLICANT: Tsang, Benjamin K
;; APPLICANT: Pratt, Christine
;; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPs AND
;; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF*PROLIFERATIVE
;; TITLE OF INVENTION: DISEASE
;; FILE REFERENCE: 07891/009004
;; CURRENT APPLICATION NUMBER: US/09/974,592


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; LENGTH: 2100
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-201-936-9

Query Match      90.7%; Score 125.2; DB 9; Length 2100;
Best Local Similarity 94.2%; Pred. No. 1.2e-30;
Matches 130; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
    |||||
Db 1438 GAGCAGCTAAGGCGCTACAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 1497
    |||||

QY 61 GCTATCGTTTTTCTCTTGTGGACATCTAGTCACCTTTGAAACAATCTGCTGAAGCAGTT 120
    |||||
Db 1498 GCTATCGTTTTTCTCTTGTGGACATCTGCGCCACTGTGAACAGTGTGCGAGAGCAGTT 1557
    |||||

QY 121 GACAAGTGTCCTCATGTGC 138
    |||||
Db 1558 GACAATGTCCCATGTGC 1575
    |||||

RESULT 7
US-09-974-592-9
; Sequence 9, Application US/09974592
; Patent No. US20020120121A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: Mackenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION AND MODULATION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592
; CURRENT FILING DATE: 2001-10-09
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 09/617,053
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: US 08/800,929
; PRIOR FILING DATE: 1997-02-13
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-974-592-9

Query Match      90.7%; Score 125.2; DB 10; Length 2691;
Best Local Similarity 94.2%; Pred. No. 1.4e-30;
Matches 130; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
    |||||
Db 1983 GAGCAGCTAAGGCGCTACAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 2042
    |||||

QY 61 GCTATCGTTTTTCTCTTGTGGACATCTAGTCACCTTTGAAACAATCTGCTGAAGCAGTT 120
    |||||
Db 2043 GCTATCGTTTTTCTCTTGTGGACATCTGCGCCACTGTGAACAGTGTGCGAGAGCAGTT 2102
    |||||

QY 121 GACAAGTGTCCTCATGTGC 138
    |||||
Db 2103 GACAATGTCCCATGTGC 2120
    |||||

RESULT 8
US-10-095-407-16/c
; Sequence 16, Application US/10095407
; Patent No. US20020164330A1
; GENERAL INFORMATION:
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; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 152331
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(152331)
; OTHER INFORMATION: n = A,T,C or G
US-10-095-407-16

Query Match      86.5%; Score 119.4; DB 9; Length 152331;
Best Local Similarity 92.0%; Pred. No. 6.6e-28;
Matches 126; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
    |||||
Db 24123 GAGCAGCTAAGACACCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 24064
    |||||

QY 61 GCTATCGTTTTTCTCTTGTGGACATCTAGTCACCTTTGAAACAATCTGCTGAAGCAGTT 120
    |||||
Db 24063 GCTGTCGTTTTTATCTCTGTCGACATCCAGTCACCTGCTAAACAATCTGCTGAAGTGGTT 24004
    |||||

QY 121 GACAAGTGTCCTCATGTGC 137
    |||||
Db 24003 GACAATGTCTCAAGTG 23987
    |||||

RESULT 9
US-10-095-407-17
; Sequence 17, Application US/10095407
; Patent No. US20020164330A1
; GENERAL INFORMATION:
; APPLICANT: Pan, Yang
; TITLE OF INVENTION: NOVEL MOLECULES OF TANGO-77 RELATED PROTEIN FAMILY
; FILE REFERENCE: 09404/052001
; CURRENT APPLICATION NUMBER: US/10/095,407
; CURRENT FILING DATE: 2002-03-11
; PRIOR APPLICATION NUMBER: US 60/091,650
; PRIOR FILING DATE: 1998-07-02
; PRIOR APPLICATION NUMBER: US 60/054,646
; PRIOR FILING DATE: 1997-08-04
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 17
; LENGTH: 176373
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(176373)
; OTHER INFORMATION: n = A,T,C or G
US-10-095-407-17

Query Match      86.5%; Score 119.4; DB 9; Length 176373;
Best Local Similarity 92.0%; Pred. No. 7e-28;
Matches 126; Conservative 0; Mismatches 11; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGGCGCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
    |||||
Db 13011 GAGCAGCTAAGACACCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 13070
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RESULT 11
US-09-974-592-13
; Sequence 13, Application US/09974592
; Patent No. US2002012012A1
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G
; APPLICANT: MacKenzie, Alexander E
; APPLICANT: Liston, Peter
; APPLICANT: Baird, Stephen
; APPLICANT: Tsang, Benjamin K
; APPLICANT: Pratt, Christine
; TITLE OF INVENTION: DETECTION OF IAPS AND
; TITLE OF INVENTION: NAIP FOR THE DIAGNOSIS AND TREATMENT OF PROLIFERATIVE
; TITLE OF INVENTION: DISEASE
; FILE REFERENCE: 07891/009004
; CURRENT APPLICATION NUMBER: US/09/974,592

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	Best Local Similarity	65.0%;	Pred. No. 1.4e-09;		
	Matches	89;	Conservative	0;	Mismatches 48; Indels 0; Gaps 0
QY	1	GAGCAGCTAAGCGCGCTGCAAGAGAGAGACCTTGC	AAATCTGTATGCATGCAATATTT	60	
DB	1785	GAAACAGTTGCGGCCCTCCCGAGGACAGAAATGTGTAAAGTGTGTATGGACCGCAGAGGTA	1844		
QY	61	GCTATCGTTTTTTTGCTTGTGGACATCTAGTCAC	TTGTAACAATGTCCTGAAGCAGTT	120	
DB	1845	TCCATCGTGTTCATTCCTCGTGGCCATCTGGTCGTG	GCAAGACATCCGCTCCCTCTCTG	1904	
QY	121	GACAAAGTGTC	CCCATGTG	137	

QY 121 GACAAGTGTCCCATGTG 137

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Db 2480 AGAAGTGTCCCATTTG 2496

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Job time : 70.1823 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

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Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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13: gb_est4:*
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15: em_estfun:*
16: em_estom:*
17: gb_gss:*
18: em_gss_hum:*
19: em_gss_inv:*
20: em_gss_pln:*
21: em_gss_vrt:*
22: em_gss_fun:*
23: em_gss_mam:*
24: em_gss_mus:*
25: em_gss_other:*
26: em_gss_pro:*
27: em_gss_rod:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
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C 3	135	97.8	784	9	AI628066	AI628066 ty84b02.x
4	130	94.2	684	13	BI739916	BI739916 603362459
5	128.4	93.0	305	10	BB489347	BB489347 BB489347
6	123.6	89.6	221	10	BB489746	BB489746 BB489746

7	123.6	89.6	306	10	BB493232	BB493232
8	123.6	89.6	308	10	BB489976	BB489976
C 9	123	89.1	447	9	AI148337	AI148337 tg48a12.x
10	122	88.4	319	10	BB491005	BB491005
11	120.4	87.2	339	10	BB495446	BB495446
C 12	118.4	85.8	560	17	AO697308	AO697308 HS_5531_B
13	115	83.3	716	10	AV706807	AV706807
14	114	82.6	218	10	BB489839	BB489839
15	114	82.6	684	17	AG124597	AG124597 Pan ttoq1
16	104.4	75.7	752	13	BI739115	BI739115 603361374
17	102.2	74.1	422	10	BF783769	BF783769
18	80	58.0	288	14	F08325	F08325 HSC20G051 n
C 19	76.2	55.2	470	17	AQ400532	AQ400532 HS_5064_A
C 20	67	48.6	392	12	BG883866	BG883866 fp23c08.x
C 21	67	48.6	634	13	BM533524	BM533524 fw96a11.x
C 22	66.6	48.3	511	12	BF610755	BF610755 de08a04.x
23	65.4	47.4	514	13	BM533684	BM533684 fw96a11.y
24	65	47.1	456	10	BE468783	BE468783 IPHDK0050
25	65	47.1	640	14	BQ097223	BQ097223 IFHDK0101
C 26	65	47.1	673	13	BJ045197	BJ045197 BJ045197
C 27	65	47.1	816	14	BQ097355	BQ097355 IFHDK0119
C 28	64.4	46.7	771	12	BF724041	BF724041 OA7r Chlc
C 29	64.4	46.7	976	9	AU091115	AU091115 AU091115
C 30	63.4	45.9	615	13	BM438676	BM438676 IPLVr0136
C 31	63.4	45.9	647	12	BF610861	BF610861 dd96h06.x
C 32	63.2	45.8	583	13	BJ097423	BJ097423 BJ097423
C 33	61.2	44.3	400	12	BF452698	BF452698 maa61f11.
C 34	61.2	44.3	451	13	BM190727	BM190727 da330c01.
C 35	61.2	44.3	467	10	AW988289	AW988289 ug05f04.y
C 36	61.2	44.3	471	9	AA172848	AA172848 mr31e05.r
C 37	61.2	44.3	522	10	BE577966	BE577966 df81d07.x
C 38	61.2	44.3	522	13	BM260985	BM260985 dag31e03.
C 39	61.2	44.3	564	13	BM191198	BM191198 da33h09.
C 40	61.2	44.3	565	10	AW640116	AW640116 bl91e04.w
C 41	61.2	44.3	568	14	BQ386511	BQ386511 NISC_mn18
C 42	61.2	44.3	597	14	BQ569086	BQ569086 q1121b06.
C 43	61.2	44.3	605	13	BM260905	BM260905 dag31e03.
C 44	61.2	44.3	618	10	BE578881	BE578881 df56h07.x
C 45	61.2	44.3	646	12	BG161881	BG161881 df69f09.x

ALIGNMENTS

RESULT 1
BF754025/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS

BF754025
CM2-CT5003-051000-408-g04 CT5003 Homo sapiens CDNA, mRNA sequence.
BF754025.1 GI:12080701
EST.
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 446)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

TITLE
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags

JOURNAL
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

MEDLINE
20202663

COMMENT
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001

Email: asimpson@ludwig.org.br
 This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL
 (http://www.ludwig.org.br/scripts/gethtml2.pl?tl=CM2&tl2=CM2-CF5003-051000-48-904&tl3=2000-10-05&tl4=1)
 Seg primer: puc 18 forward
 High quality sequence start: 6
 High quality sequence stop: 446.

FEATURES

source

1. 446
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_lib="CF5003"
 /dev_stage="Adult"

/note="Organ: colon; Vector: puc18; Site 1: SmaI; Site 2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 156 716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 145 a 94 c 69 g 138 t
 ORIGIN

Query Match 100.0%; Score 138; DB 12; Length 446;
 Best Local Similarity 100.0%; Pred. No. 6.9e-32;
 Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTCCAAATCTGTATGATAGAATATT 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 358 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTCCAAATCTGTATGATAGAATATT 299
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 GCTATCGTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGTCTGAAGCAGTT 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 298 GCTATCGTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGTCTGAAGCAGTT 239
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 GACAAGTGCCCATGTGC 138
 ||||||||||||||||||
 Db 238 GACAAGTGCCCATGTGC 221
 ||||||||||||||||||

RESULT 2

BQ007511/c

LOCUS

DEFINITION BQ007511 757 bp mRNA linear EST 26-MAR-2002
 UI-H-ED1-ayb-b-04-0-UI-s1 NCI-CGAP_ED1 Homo sapiens CDNA clone
 IMAGE:5836323 3', mRNA sequence.

ACCESSION

BQ007511

VERSION

BQ007511.1

KEYWORDS

EST.

SOURCE

human.

ORGANISM

Homo sapiens

REFERENCE

1 (bases 1 to 757)

AUTHORS

NCI-CGAP

TITLE

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

JOURNAL

Contact: Robert Strausberg, Ph.D.

COMMENT

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Jose Mercuende

CDNA Library Preparation: Dr. M. Bento Soares, University of Iowa

DNA Sequencing by: Dr. M. Bento Soares, University of Iowa

Clone Distribution: Dr. M. Bento Soares, University of Iowa

Through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Seg primer: M13 FORWARD

POLYA=Yes.

Location/Qualifiers

1. 757

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:5836323"

/clone_lib="NCI-CGAP_ED1"
 /tissue_type="Chondrosarcoma"
 /dev_stage="Adult"

/lab_host="DH10B (Life Technologies)"

/note="Organ: Left Pubic Bone; Vector: pT7T3-Pac

(Pharmacia) with a modified polylinker; Site 1: EcoR I;

Site 2: Not I; NCI-CGAP_ED1 is a normalized CDNA library

containing the following tissue(s): Chondrosarcoma cell

line C85. The library was constructed according to Bonaldo

, Lennon and Soares, Genome Research, 6:791-806, 1996.

First strand cDNA synthesis was primed with an oligo-dT

primer containing a Not I site. Double stranded cDNA was

cloned directionally into pT7T3-Pac vector. The

oligonucleotide used to prime the synthesis of

first-strand cDNA contains a library tag sequence that is

located between the Not I site and the (GT)₁₈ tail. The

sequence tag for this library is GCTCAAGGCT.

TAG-LIB-UI-H-ED1

TAG-TISSUE=Chondrosarcoma

TAG_SEQ=CGTCAAGGCT"

BASE COUNT 257 a 141 c 105 g 254 t

ORIGIN

Query Match 100.0%; Score 138; DB 14; Length 757;

Best Local Similarity 100.0%; Pred. No. 8.4e-32;

Matches 138; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTCCAAATCTGTATGATAGAATATT 60

|||||

Db 653 GAGCAGCTAAGCGCCTGCAAGAGGAGAGCTTTCCAAATCTGTATGATAGAATATT 594

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QY 61 GCTATCGTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGTCTGAAGCAGTT 120

|||||

Db 593 GCTATCGTTTTGTTCCTTGTGGACATCTAGTCACCTTGTAAACAATGTCTGAAGCAGTT 534

|||||

QY 121 GACAAGTGCCCATGTGC 138

|||||

Db 533 GACAAGTGCCCATGTGC 516

|||||

RESULT 3

AI628066/c

LOCUS

DEFINITION AI628066 784 bp mRNA linear EST 07-MAR-2000

TS94B02.X1 NCI-CGAP_Kid11 Homo sapiens CDNA clone IMAGE:2285739 3',

similar to SW-1AP3_HUMAN P98170 INHIBITOR OF APOPTOSIS PROTEIN 3 ; ,

mRNA sequence.

ACCESSION AI628066

VERSION AI628066.1

KEYWORDS GI:4664866

EST.

SOURCE human.

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

1 (bases 1 to 784)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),

Tumor Gene Index

Unpublished (1997)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.

Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: M. Bento Soares, Ph.D.

CDNA Sequencing by: Greg Lennon, Ph.D.

Clone Distribution: Washington University Genome Sequencing Center

Through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

Seg primer: -400P from Gibco

High quality sequence stop: 466

POLYA=No.

Location/Qualifiers

1. 784

/organism="Homo sapiens"

/db_xref="taxon:9606"

/clone="IMAGE:2285739 3"

Site_2: Sali; Cloned unidirectionally; oligo-dT primed.
Average insert size 3.3 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library.*

BASE COUNT	202 a	121 c	148 g	213 t
ORIGIN				
Query Match	94.2%; Score 130; DB 13; Length 684;			
Best Local Similarity	96.4%; Pred. No. 2.3e-29;			
Matches 133; Conservative	0; Mismatches 5; Indels 1; Gaps 0;			
QY	1 GAGCAGCTAAGGGCCGTCGAAGAGGAGAAGCTTTGGCAAAATCTGTATGGATAGAAAATT 60			
DB				
QY	70 GAGCAGCTAAGGGCCGTCGAAGAGGAGAAGCTTTGGCAAAATCTGTATGGATAGAAAATT 129			
DB				
QY	61 GCATCGTTTTTGTCCTTGTGGACATCTAGTCACTTGTAAACAATGCTGCTGAAGCAGTT 120			
DB				
QY	130 GCTATCGTTTTTGTCCTTGTGGACATCTAGTCACTTGTAAACAAGTGGCAGAGCAGTT 189			
DB				
QY	121 GACAAGTGTCCTCATGTGC 138			
DB				
QY	190 GACAATGTCCCATGTGC 207			
DB				
RESULT 5				
BB489347	305 bp mRNA linear EST 23-JUL-2000			
LOCUS	BB489347 RIKEN full-length enriched, 13 days embryo stomach Mus			
DEFINITION	musculus cDNA clone D53006021.3 similar to U36942 Mus musculus			
ACCESSION	IAP homolog A (MIRA) mRNA, mRNA sequence.			
VERSION	BB489347.1 GI:9406956			
KEYWORDS	EST.			
SOURCE	house mouse.			
ORGANISM	Mus musculus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
AUTHORS	1 (bases 1 to 305) Konno,H., Alzawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,T., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Koijima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Mikai,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saïto,H., Sakai,C., Sato,K., Shibata,K., Shibata, Y., Shigenoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takehashi,F., Tomimaga,N., Toya, T., Tsunoda,Y., Watanahi,A., Watanabe,S., Yamamura,T., Yamanaka,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino, M., Muramatsu,M. and Hayashizaki,Y. RIKEN Mouse ESTs (Konno,H., et al.) Unpublished (2000)			
TITLE	Contact: Yoshihide Hayashizaki			
JOURNAL	Laboratory for Genome Exploration Research Group, RIKEN Genomic			
COMMENT	Sciences Center(GSC), Yokohama Institute The Institute of Physical and Chemical Research (RIKEN) 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan Tel.: 81-45-503-9222 Fax: 81-45-503-9216 Email: genome-resgsc.riken.go.jp/ URL:http://genome-gsc.riken.go.jp/ Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoaka,S., Sasakawa, N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y. Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998) Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki, Y. and Hayashizaki,Y. Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999) Carninci,P. and Hayashizaki,Y. High-efficiency full-length cDNA cloning. Methods Enzymol. 303,			

19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES
source
Location/Qualifiers
1..305
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="RIKEN full-length enriched, 13 days embryo stomach"
/tissue_type="stomach"
/dev_stage="13 days embryo"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'.
GAGAGAGAGCGCGCAACTCGAGTGTTCCTTTTTCCTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'.
GAGAGAGATTCGAGTTAATAATTAATCCCGCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT
89 a 65 c 68 g 83 t

ORIGIN
Query Match 93.0%; Score 128.4; DB 10; Length 305;
Best Local Similarity 95.7%; Pred. No. 5.4e-29;
Matches 132; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 1 GAGCAGCTAAGCGCGCTGCAAGAGAGAGAGCGTTTGCATAATCTGTATGATAGAAATATT 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 146 GAGCAGCTAAGCGCGCTGCAAGAGAGAGAGCGTTTGCATAATCTGTATGATAGAAATATT 205
Qy 61 GCTATCGTTTTTGTTCCTTGTGACATCTAGTCACCTGTGAACAATGTGCTGAACAGGTT 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 206 GCTTCGTTTTTGTTCCTTGTGACATCTAGTCACCTGTGAACAATGTGCTGAACAGGTT 265
Qy 121 GACAAAGTGTCCCATGTGC 138
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 266 GACAAAGTGTCCCATGTGC 283
RESULT 6
BB489746 221 bp mRNA linear EST 23-JUL-2000
BB489746 RIKEN full-length enriched, 13 days embryo stomach Mus
musculus cDNA clone D53009D11 3' similar to U36842 Mus musculus
IAP homolog A (MIHA) mRNA, mRNA sequence.

ACCESSION
BB489746
VERSION
BB489746.1 GI:9407355
KEYWORDS
EST.
SOURCE
house mouse.
Mus musculus

ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 221)
Konno.H., Aizawa.K., Akahira.S., Akiyama.J., Hara.A., Hayatsu.N.,
P., Endo.T., Fukuda.S., Fukunishi.Y., Hara.A., Hayatsu.N., Itoh.M.,
Hirozane.T., Hori.F., Ishii.Y., Ishikawa.J., Ishikawa.T., Itoh.M.,
Izawa.M., Kadota.K., Kagawa.I., Kai.C., Kawai.J., Kikuchi.N.,
Kiyosawa.H., Kojima.Y., Kondo.S., Koya.S., Kurihara.C., Kusakabe.M.,
Matsuyama.T., Miki.R., Mizuno.Y., Nakamura.M., Oda.H., Okazaki.Y.,
Ono.T., Owa.C., Saito.H., Sakai.C., Sato.K., Shibata.K., Shibata.Y.,
Shigenoto.Y., Shinagawa.A., Shiraki.T., Sogabe.Y., Sugahara.Y.,
Suzuki.H., Suzuki.H., Tagawa.A., Takahashi.F., Tomimaga.N., Toya.T., Tsunoda.Y., Watahiki.A., Watanabe.S., Yamamura.T., Yamanaka.I.,
Yano.R., Yasunishi.A., Yokota.T., Yoshida.K., Yoshiki.A., Yoshino

M., Muramatsu,M. and Hayashizaki,Y.
RIKEN Mouse ESTs (Konno.H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic
Sciences Center(GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp.
URL: <http://genome-gsc.riken.go.jp/>
Carninci.P., Nishiyama.Y., Westover.A., Itoh.M., Nagaoaka.S., Sasaki
N., Okazaki.Y., Muramatsu,M. and Hayashizaki,Y.
Thermostabilization and thermoactivation of thermostable enzymes by
trehalose and its application for the synthesis of full length
cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2), 520-524 (1998)
Itoh.M., Kitsuai.T., Akiyama.J., Shibata.K., Izawa.M., Kawai.J.,
Tomaru.Y., Carninci.P., Shibata.Y., Ozawa.Y., Muramatsu,M., Okazaki
Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation
system. Genome Res. 9 (5), 463-470 (1999)
Carninci.P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES
Location/Qualifiers
1..221
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone_lib="RIKEN full-length enriched, 13 days embryo stomach"
/tissue_type="stomach"
/dev_stage="13 days embryo"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5'.
GAGAGAGAGCGCGCAACTCGAGTGTTCCTTTTTCCTTNN 3']. cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5'.
GAGAGAGATTCGAGTTAATAATTAATCCCGCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT
67 a 50 c 45 g 59 t

ORIGIN
Query Match 89.6%; Score 123.6; DB 10; Length 221;
Best Local Similarity 93.5%; Pred. No. 1.4e-27;
Matches 129; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GAGCAGCTAAGCGCGCTGCAAGAGAGAGAGCGTTTGCATAATCTGTATGATAGAAATATT 60
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 61 GAGCAGCTAAGCGCGCTGCAAGAGAGAGAGCGTTTGCATAATCTGTATGATAGAAATATT 120
Qy 61 GCTATCGTTTTTGTTCCTTGTGACATCTAGTCACCTGTGAACAATGTGCTGAACAGGTT 120
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 121 GCTATCGTTTTTGTTCCTTGTGACATCTAGTCACCTGTGAACAATGTGCTGAACAGGTT 180
Qy 121 GACAAAGTGTCCCATGTGC 138
||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
Db 181 GACAAATATCCCATGTGC 198
RESULT 7

[illegible]

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES

Location/Qualifiers
1..308
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="DS30012B15"
/clone_lib="RIKEN full-length enriched, 13 days embryo stomach"
/tissue.type="stomach"
/dev_stage="13 days embryo"
/lab_host="DH10B"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGCGCGCACTCGAGTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGTTAATTAATTAATCCGCCGCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT
88 a 68 c 67 g 85 t

Query Match 89.6%; Score 123.6; DB 10; Length 308;
Best Local Similarity 93.5%; Pred. No. 1.6e-27;
Matches 129; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GAGCAGCTAAGCGCTCGAAGAGAGAGAGCTTCCAAAATCTGTATGATAGAAATATT 60
|||||
Db 148 GACCAGCTAAGCGCTCAAGAGAGAGAGCTTCCAAAATCTGTATGATAGAAATATT 207
|||||

Qy 61 GCTATCGTTTTTGTCTGTGACATCTAGTCACCTTGTAAACAATGCTGAAGCAGCTT 120
|||||
Db 208 GCTTTCGTTTTTGTCTGTGACATCTGTTCACCTTGTAAACAATGCTGAAGCAGCTT 267
|||||

Qy 121 GACAAATGCCCATGTC 138
|||||
Db 268 GACAAATGCCCATGTC 285
|||||

RESULT 9
A1418337/c
LOCUS
DEFINITION
t948a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:211198 3' similar to gb:X55110 MIDKINE PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION
A1418337
VERSION
A1418337.1 GI:4264268
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: 40up from Gibco
High quality sequence stop: 435.
Location/Qualifiers
1..447

us-09-654-743-48.rst

Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

Location/Qualifiers
1..308
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="DS30012B15"
/clone_lib="RIKEN full-length enriched, 13 days embryo stomach"
/tissue.type="stomach"
/dev_stage="13 days embryo"
/lab_host="DH10B"
/note="Site 1: SalI; Site 2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5', GAGAGAGAGCGCGCACTCGAGTTTTTTTTTTTNN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATTCGAGTTAATTAATTAATCCGCCGCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC I."

BASE COUNT
88 a 68 c 67 g 85 t

Query Match 89.6%; Score 123.6; DB 10; Length 308;
Best Local Similarity 93.5%; Pred. No. 1.6e-27;
Matches 129; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

Qy 1 GAGCAGCTAAGCGCTCGAAGAGAGAGAGCTTCCAAAATCTGTATGATAGAAATATT 60
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Db 148 GACCAGCTAAGCGCTCAAGAGAGAGAGCTTCCAAAATCTGTATGATAGAAATATT 207
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Qy 61 GCTATCGTTTTTGTCTGTGACATCTAGTCACCTTGTAAACAATGCTGAAGCAGCTT 120
|||||
Db 208 GCTTTCGTTTTTGTCTGTGACATCTGTTCACCTTGTAAACAATGCTGAAGCAGCTT 267
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Qy 121 GACAAATGCCCATGTC 138
|||||
Db 268 GACAAATGCCCATGTC 285
|||||

RESULT 9
A1418337/c
LOCUS
DEFINITION
t948a12.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:211198 3' similar to gb:X55110 MIDKINE PRECURSOR (HUMAN);, mRNA sequence.

ACCESSION
A1418337
VERSION
A1418337.1 GI:4264268
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 447)
NCI-CCAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgaps-remail.nih.gov
This clone is available royalty-free through LINL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: 40up from Gibco
High quality sequence stop: 435.
Location/Qualifiers
1..447

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:211198"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Equal amounts of plasmid DNA from three normalized libraries (fetal lung NBHL19W, testis NHT, and B-cell NCI-CGAP-GCB1) were mixed, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from pools of 5,000 clones made from the same 3 libraries. The pools consisted of I.M.A.G.E. clones 297480-302087, 582632-687239, 726408-728711, and 729096-731399. Subtraction by Bento Soares and M. Fatima Bonaldo."

BASE COUNT
160 a 75 c 69 g 143 t

ORIGIN

Query Match 89.1%; Score 123; DB 9; Length 447;
Best Local Similarity 100.0%; Pred. No. 2.8e-27;
Matches 123; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 16 CTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATTCATCGTTTTTGT 75
|||||
Db 447 CTGCAAGAGGAGAGCTTTGCAAAATCTGTATGGATAGAAATATTCATCGTTTTTGT 388
|||||

Qy 76 CTTTGTGACATCTAGTCACCTTTGTAACAATCTGCTGAAGCAGCTTGCACAGTGCCCATG 135
|||||
Db 367 CTTTGTGACATCTAGTCACCTTTGTAACAATCTGCTGAAGCAGCTTGCACAGTGCCCATG 328
|||||

Qy 136 TGC 138
|||

Db 327 TGC 325
|||

RESULT 10
BB491005
LOCUS
DEFINITION
BB491005 RIKEN full-length enriched, 13 days embryo stomach Mus musculus cDNA clone D530019A07 3' similar to U36842 Mus musculus IAP homolog A (MHA) mRNA, mRNA sequence.

ACCESSION
BB491005
VERSION
BB491005.1 GI:9449632
KEYWORDS
EST.
SOURCE
house mouse.
ORGANISM
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 319)
Konno.H., Aizawa.K., Akahira.S., Akiyama.J., Arakawa.T., Carninci.P., Endo.T., Fukuda.S., Fukunishi.Y., Hara.A., Hayatsu.N., Hirozane.T., Hori.F., Ishii.Y., Ishikawa.J., Ishikawa.T., Itoh.M., Izawa.M., Kadota.K., Kagawa.I., Kai.C., Kawai.J., Kikuchi.N., Kiyosawa.H., Kojima.Y., Kondo.S., Koya.S., Kurihara.C., Kusakabe.M., Matsuyama.T., Miki.R., Mizuno.Y., Nakamura.M., Oda.H., Okazaki.Y., Ono.T., Owa.C., Saito.H., Sakai.C., Sato.K., Shibata.K., Shibata.Y., Shigemoto.Y., Shinagawa.A., Shiraki.T., Sogabe.Y., Sugahara.Y., Suzuki.H., Suzuki.H., Tagawa.A., Takahashi.F., Tomimaga.N., Toya.T., Tsunoda.Y., Watahiki.A., Watanabe.S., Yamamuta.T., Yamana.K., Yano.R., Yasunishi.A., Yokota.T., Yoshida.K., Yoshiki.A., Yoshino.M., Muramatsu.M. and Hayashizaki.Y.
RIKEN Mouse ESTs (Konno.H., et al.)
Unpublished (2000)
Contact: Yoshihide Hayashizaki
Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), Yokohama Institute
The Institute of Physical and Chemical Research (RIKEN)
1-7-22 Suenho-cho, Tsukumi-ku, Yokohama, Kanagawa 230-0045, Japan
Tel: 81-45-503-9222
Fax: 81-45-503-9216
Email: genome-res@gsc.riken.go.jp.

URL:<http://genome.gsc.riken.go.jp/Carninci,P.,Nishiya,Y.,Westover,A.,Itoh,M.,Nagaoka,S.,Sasaki,N.,Okazaki,Y.,Muramatsu,M.andHayashizaki,Y.>
Thermotabilization and thermoactivation of the thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)
Itoh,M.,Y. Katsunai,T.,Akiyama,J.,Shibata,K.,Izawa,M.,Kawai,J.,Tomaru,Y.,Carninci,P.,Shibata,Y.,Ozawa,Y.,Muramatsu,M.,Okazaki,Y. and Hayashizaki,Y.
Automated filtration-based high-throughput plasmid preparation system. *Genome Res.* 9 (5), 463-470 (1999)
Carninci,P. and Hayashizaki,Y.
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 303, 19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for further details.

FEATURES
SOURCE

Location/Qualifiers
1. 319
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="D530019A07"
/clone.lib="RIKEN full-length enriched, 13 days embryo stomach"
/tissue_type="stomach"
/dev_stage="13 days embryo"
/lab_host="DH10B"
/note="Site.1: Salt; Site.2: BamHI; cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN, Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. 1st strand cDNA was primed with a primer [5',
GAGAGAGAGCGCGCGACATCGAGTTTCTTTTCTTTTCTT 3'], cDNA was prepared by using tri-nalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5',
GAGAGAGAGATTCCTCGAGTTAATTAATTAATCCCGCCCCCCCC 3']. cDNA was cleaved with BamHI and XhoI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FLC 1." 86 c . 60 g 92 t

BASE COUNT

ORIGIN

	Query Match	88.4%	Score 122;	DB 10;	Length 319;
	Best Local Similarity	92.8%;	Pred. No. 5.le-27;		
	Matches 128;	Conservative 0;	Mismatches 10;	Indels 0;	Gaps 0;
Qy	1	GAGCAGCTAAGGCCCTGCTCAAGAGGAGAGCGTTTGCACAAATCTGTATGGATAGAATAATT	60		
Dd	159	GAGCACCTTAAGGCCCTCAAGAGGAGAGCGTTCACAAATCTGTATGGATAGAATAATT	218		
Qy	61	GCTATCGTTTTTTTGTCCTGTGGACATCTAGTCACCTTTAAACAATGTGCTGAACGAGTT	120		
Dd	219	GCTTTCCGTTTTTGTTCCTGTGGACTTCTGGTCACCTTTAAACAGTGTGCAGAAGCAGTT	278		
Qy	121	GACAAAGTGTCCCAGTGC	138		
Dd	279	GACAAATGTCCCATGTGC	296		

RESULT 11	BB495446	339 bp	mRNA	linear	EST 26-JUL-2000
LOCUS	BB495446				
DEFINITION	BB495446 RIKEN full-length enriched, 13 days embryo stomach Mus musculus cDNA clone D530048F15 3', similar to U36842 Mus musculus IAP homolog A (MIHA) mRNA, mRNA sequence.				
ACCESSION	BB495446				
VERSION	BB495446.1	GI:9467264			
KEYWORDS	EST				
SOURCE	house mouse.				
ORGANISM	Mus musculus				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				

REFERENCE
AUTHORS

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 339)

Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M., Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N., Kiyosawa,H., Kojima,Y., Kondo,S., Koya,S., Kurihara,C., Kusakabe,M., Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y., Ono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata,Y., Shigemoto,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Sugahara,Y., Suzuki,H., Suzuki,H., Tagawa,A., Takahashi,F., Tominaga,N., Toyota,T., Tsunoda,Y., Watanabe,A., Watanabe,S., Yamamura,T., Yamano,I., Yano,R., Yasunishi,A., Yokota,T., Yoshida,K., Yoshiki,A., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.

RIKEN Mouse ESTs (Konno,H., et al.)

Unpublished (2000)

Contact: Yoshihide Hayashizaki

Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center(GSC), Yokohama Institute

The Institute of Physical and Chemical Research (RIKEN)

1-7-22 Suehiro-cho, Tsurumi-Ku, Yokohama, Kanagawa 230-0045, Japan

Tel: 81-45-503-9222

Fax: 81-45-503-9216

Email: genome-res@gsc.riken.go.jp/
URL:<http://genome.gsc.riken.go.jp/>

Carninci,P., Nishiyama,Y., Westover,A., Itoh,M., Nagaoka,S., Sasakawa,N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.

Thermotabilization and thermoactivation of thermolabile enzymes by trehalose and its application for the synthesis of full length cDNA. Proc. Natl. Acad. Sci. U.S.A. 95 (2) 520-524 (1998)

Itoh,M., Kitsunai,T., Akiyama,J., Shibata,K., Izawa,M., Kawai,J., Tomaru,Y., Carninci,P., Shibata,Y., Ozawa,Y., Muramatsu,M., Okazaki,Y. and Hayashizaki,Y.

Automated filtration-based high-throughput plasmid preparation system. Genome Res. 9 (5), 463-470 (1999)

Carninci,P. and Hayashizaki,Y.

High-efficiency full-length cDNA cloning. Methods Enzymol. 303, 19-44 (1999)

Please visit our web site (<http://genome.rtc.riken.go.jp/>) for further details.

FEATURES SOURCE

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Location/Qualifiers
1. .339
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="D530048F15"
/clone_lib="RIKEN full-length enriched, 13 days embryo
stomach"
/tissue_type="stomach"
/dev_stage="13 days embryo"
/lab_host="DH10B"
/note="Site_1: SalI; Site_2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN, Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
primed with a primer [5',
GAGAGAGAGCGCGCCGACCTCAGCTTTTTTTTTTTNN 3'], cDNA was
prepared by using trehalose thermo-activated reverse
transcriptase and subsequently enriched for full-length by
cap-trapper. Second strand cDNA was prepared with the
primer adapter of sequence [5',
GAGAGAGAGATCTCGAGTTAATTAATAATATCCCGCCCCCCC 3']. cDNA
was cleaved with BamHI and XhoI. Vector: a modified
pBluescript KS(+) after bulk excision from Lambda FLC I."
94 a 90 c 56 g 99 t
87.2%; Score 120.4; DB 10; Length 339;
127; Similarity 92.0%; Pred No. 1,6e-26;
Conservative 0; Mismatches 11; Indels 0; Gaps 0
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Query Mat
Best Loca

1 GAGCAGCTAAGCGCCCTGCAAGAGGAGAGCTTTCAAAATCTGTATGGATAGAAATATT 60

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Db 180 GACCAGCTAAGGCCCTTACAAAGAGAGAAAGCTTTCCAAAATCTGTATGGATAGAAATATT 239
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Db 240 GCCTTCGTTTGTTCCTTGTGGACATCTGTCCTACTTGTAAACAGTGTGCAGAACGAGTT 299
QY 121 GACAAGTGTCCCATGTGC 138
Db 300 GACAAATTTCCCATGTGC 317

RESULT 12
LOCUS AQ697308/c
DEFINITION HS 5531.B1.D07.T7A RPCI-11 Human Male BAC Library Homo sapiens
ACCESSION AQ697308
VERSION genomic clone Plate-1107 Col-13 Row-H, DNA sequence.
KEYWORDS GSS.
SOURCE Homo sapiens
ORGANISM human.
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 560)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1107 row: H column: 13
Seq primer: T7
Class: BAC ends
High quality sequence stop: 560.
FEATURES
Location/Qualifiers
1..560
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Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"
BASE COUNT 154 a 121 c 90 g 187 t 8 others
ORIGIN
Query Match 85.8%; Score 118.4; DB 17; Length 560;
Best Local Similarity 91.2%; Pred. No. 8e-26;
Matches 125; Conservative 0; Mismatches 12; Indels 0; Gaps 0;
QY 1 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 60
Db 299 GAGCAGCTAAGCAGCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 240
QY 61 GCTATCGTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGCTGCTGAAGCAGTT 120

```

```

Db 239 GCTCGCTTTTATTCCTTGTGGACATCCAGTCACTCTGTAACAATGCTGCTGAAGTGGT 180
QY 121 GACAAGTGTCCCATGTG 137
Db 179 GACAAATGCTCTCAAGTG 163

RESULT 13
LOCUS AV706807
DEFINITION AV706807 ADB Homo sapiens cDNA clone ADBCOF01 5', mRNA sequence.
ACCESSION AV706807
VERSION AV706807.1 GI:10724085
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 716)
Peng,Y., Song,H., Huang,Q., Huang,C., Gu,Y., Yang,Y., Gao,G., Xiao
,H., Xu,X., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z.,
Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M., Lu
,G., Hu,R., Chen,J., Chen,Z. and Han,Z.
Homo sapiens cDNA ADB clones
Unpublished (2000)
Contact: Zeguang Han
Chinese National Human Genome Center at Shanghai
351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
201203, P. R. China
Tel: 86-21-50801919(ex.45)
Fax: 86-21-50801922
Email: hanzeg@hgc.sh.cn
This clone is available at CHGC in Shanghai.
FEATURES
Location/Qualifiers
1..716
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XhoI"
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Best Local Similarity 93.5%; Pred. No. 9.7e-25;
Matches 129; Conservative 0; Mismatches 8; Indels 1; Gaps 1;
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Db 515 GAGCAGCTAAGCGCCTGCAAGAGGAGAGAGCTTTGCAAAATCTGTATGGATAGAAATATT 574
QY 61 GCTATCGTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGCTGCTGAAGCAGTT 120
Db 575 GCTATCGTTTGTTCCTTGTGGACATCTAGTCACTTGTAAACAATGCTGCTGAAGCAGTT 633
QY 121 GACAAGTGTCCCATGTGC 138
Db 634 GACACGTGTNCCATGTGC 651

RESULT 14
LOCUS BB489839
DEFINITION BB489839 RIKEN full-length enriched, 13 days embryo stomach Mus
musculus cDNA clone D530010E15 3' similar to U36842 Mus musculus
IAP homolog A (MIHA) mRNA, mRNA sequence.
ACCESSION BB489839
VERSION BB489839.1 GI:9407448

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KEYWORDS SOURCE ORGANISM

EST.
house mouse.
Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 218)
Konno,H., Aizawa,K., Akahira,S., Akiyama,J., Arakawa,T., Carninci
P., Endo,T., Fukuda,S., Fukunishi,Y., Hara,A., Hayatsu,N., Itochi
Hirozane,T., Hori,F., Ishii,Y., Ishikawa,J., Ishikawa,T., Itoh,M.,
Izawa,M., Kadota,K., Kagawa,I., Kai,C., Kawai,J., Kikuchi,N.,
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Matsuyama,T., Miki,R., Mizuno,Y., Nakamura,M., Oda,H., Okazaki,Y.,
Oono,T., Owa,C., Saito,H., Sakai,C., Sato,K., Shibata,K., Shibata
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T., Tsunoda,F., Wachihi,A., Watanabe,S., Yamamura,T., Yamanaka,I.,
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The Institute of Physical and Chemical Research (RIKEN)
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Email: genome-res@gs.riken.go.jp,
URL: http://genome.gsc.riken.go.jp/
N., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
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High-efficiency full-length cDNA cloning. Methods Enzymol. 303,
19-44 (1999)
Please visit our web site (<http://genome.rtc.riken.go.jp>) for
further details.

TITLE JOURNAL COMMENT

AG124597
Pan troglodytes DNA, clone: PTB-134J15.F, genomic survey sequence.
AG124597
AG124597.1 GI:16653762
GSS.
Pan troglodytes male lymphoblast DNA, clone: PTB-134J15.F.
BAC Library clone: PTB-134J15.F.
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
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BAC end sequences of Library PTB
Unpublished
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(E-mail: chimb@gs.riken.go.jp, URL: <http://hgp.gsc.riken.go.jp/>,
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Clones are derived from the chimpanzee BAC library PTB this BAC end
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REFERENCE

AUTHORS
TITLE
JOURNAL
AUTHORS
TITLE
JOURNAL
COMMENT

COMMENT

Sequencing: -21M13
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FEATURES source

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/note="Site 1: SalI; Site 2: BamHI; cDNA library was
prepared and sequenced in Mouse Genome Encyclopedia
Project of Genome Exploration Research Group in Riken
Genomic Sciences Center and Genome Science Laboratory in
RIKEN. Division of Experimental Animal Research in Riken
contributed to prepare mouse tissues. 1st strand cDNA was
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GAGAGAGAGCGCGCCGCACTCGAGTTTCTTTTCTTTT 3'], cDNA was
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pBluescript KS(+) after bulk excision from Lambda FLC I."
61 a 52 c 38 g 67 t

BASE COUNT ORIGIN

Query Match
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QY 61 GCTATCGTTTTTGTCTTGTGACATCTAGTCACCTGTGTAACAAATGCTGCAAGCAGTT 120
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DB 407 GCTGTGTTTTTATCTTCCTGCGACATCTGGTCACTTGTGTAACAAATGCTGCAAGCAGTT 466

Best Local Similarity 89.1%; Pred. No. 1.3e-24;
Matches 123; Conservative 0; Mismatches 15; Indels 0; Gaps 0;

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QY 121 GACAAGTGTCCCATGTGC 138
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DB 179 GACAAATTTCCCATGTGC 196
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RESULT 15

AG124597
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/organism="Mus musculus"
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/dev_stage="13 days embryo"
/lab_host="DH10B"
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QY 121 GACAAAGTGTCCCATGTGC 138
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Db 467 GACAGATGTCCCATGTGC 484

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